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NEWS 2		"Ask CAS" for self-help around the clock
NEWS 3	JAN 17	Pre-1988 INPI data added to MARPAT
NEWS 4	FEB 21	STN AnaVist, Version 1.1, lets you share your STN AnaVist visualization results
NEWS 5	FEB 22	The IPC thesaurus added to additional patent databases on STN
NEWS 6	FEB 22	Updates in EPFULL; IPC 8 enhancements added
NEWS 7	FEB 27	New STN AnaVist pricing effective March 1, 2006
NEWS 8	MAR 03	Updates in PATDPA; addition of IPC 8 data without attributes
NEWS 9	MAR 22	EMBASE is now updated on a daily basis
NEWS 10	APR 03	New IPC 8 fields and IPC thesaurus added to PATDPAFULL
NEWS 11	APR 03	Bibliographic data updates resume; new IPC 8 fields and IPC thesaurus added in PCTFULL
NEWS 12	APR 04	STN AnaVist $500 visualization usage credit offered
NEWS 13	APR 12	LINSPEC, learning database for INSPEC, reloaded and enhanced
NEWS 14	APR 12	Improved structure highlighting in FQHIT and QHIT display in MARPAT
NEWS 15	APR 12	Derwent World Patents Index to be reloaded and enhanced during second quarter; strategies may be affected
NEWS 16	MAY 10	CA/CAplus enhanced with 1900-1906 U.S. patent records
NEWS 17	MAY 11	KOREAPAT updates resume
NEWS 18	MAY 19	Derwent World Patents Index to be reloaded and enhanced
NEWS 19	MAY 30	IPC 8 Rolled-up Core codes added to CA/CAplus and USPATFULL/USPAT2
NEWS 20	MAY 30	The F-Term thesaurus is now available in CA/CAplus
NEWS 21	JUN 02	The first reclassification of IPC codes now complete in INPADOC
NEWS EXPRESS		FEBRUARY 15 CURRENT VERSION FOR WINDOWS IS V8.01a, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005. V8.0 AND V8.01 USERS CAN OBTAIN THE UPGRADE TO V8.01a AT http://download.cas.org/express/v8.0-Discover/
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FILE 'HOME' ENTERED AT 19:01:58 ON 06 JUN 2006

=> fil medline biosis caplus scisearch embase wpids
COST IN U.S. DOLLARS SINCE FILE ENTRY TOTAL SESSION
FULL ESTIMATED COST 0.21 0.21

FILE 'MEDLINE' ENTERED AT 19:02:22 ON 06 JUN 2006

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FILE 'WPIDS' ENTERED AT 19:02:22 ON 06 JUN 2006
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=> siRNA and librar? and random? and (hairpin (s) primer)
L1 5 SIRNA AND LIBRAR? AND RANDOM? AND (HAIRPIN (S) PRIMER)

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2 4 DUP REM L1 (1 DUPLICATE REMOVED)

=> d ibib abs l2 1-4

L2 ANSWER 1 OF 4 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2005-522573 [53] WPIDS
DOC. NO. NON-CPI: N2005-426855
DOC. NO. CPI: C2005-158574
TITLE: Preparing interfering RNA RNAi **library** from target DNA e.g. cDNA of specific gene or cDNA **library**, by cleaving target DNA, linking **hairpin** adapter to end of DNA fragments and **primer** extension reaction to produce RNAi construct.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): HIROSE, K; IINO, M; NAMIKI, S; SHIRANE, D; SUGAO, K
PATENT ASSIGNEE(S): (TOUD-N) TOUDAI TLO LTD
COUNTRY COUNT: 108
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2005063980	A1	20050714	(200553)*	JA	55

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IS IT KE LS LT LU MC MW MZ NA NL OA PL PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE

DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG
KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ
OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG
US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2005063980	A1	WO 2004-JP19612	20041228

PRIORITY APPLN. INFO: US 2003-533854P 20031231
AN 2005-522573 [53] WPIDS
AB WO2005063980 A UPAB: 20050818
NOVELTY - Preparing (M1) an interfering RNA (RNAi) **library** from a target DNA, comprising cleaving the target DNA at **random** to produce DNA fragments, linking **hairpin** adapter to one end of the DNA fragments, carrying out **primer** extension reaction using a polymerase having strand-displacement activity, and producing iRNA expression construct encoding iRNA, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) RNAi **library** (I) prepared by (M1);

(2) screening small interfering RNA (**siRNA**) expression construct having RNAi activity from (I), comprising:

(a) introducing (I) into a cell into which the target DNA is to be expressed and measuring the expression of target DNA; or

(b) introducing (I) into a cell in which a fused gene of target DNA and negative marker gene are expressed, and selecting the cell having RNAi effect using the marker; and

(3) a system (II) for preparing RNAi **library**, comprising a hairpin adapter and a double-stranded adapter, and restriction enzyme recognition site in any one of the adapters.

USE - (M1) is useful for preparing RNAi **library** from target DNA such as cDNA of specific gene or cDNA **library**. (I) is useful for screening a **siRNA** expression construct having RNAi activity. (All claimed.)

ADVANTAGE - (M1) enables to prepare an RNAi **library** having effective RNAi activity.

Dwg.0/5

L2 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2004:80858 CAPLUS
DOCUMENT NUMBER: 140:140656
TITLE: Construction of small interfering RNA expression cassettes and expression **libraries** under control of a single RNA polymerase III promoter using a polymerase **primer hairpin** linker
INVENTOR(S): Li, Henry; Chatterton, Jon E.; Ke, Ning; Rhoades, Kristina L.; Wong-Staal, Flossie
PATENT ASSIGNEE(S): Immusol Incorporated, USA
SOURCE: PCT Int. Appl., 73 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004009796	A2	20040129	WO 2003-US23239	20030723

WO 2004009796 A3 20050317
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
CA 2493251 AA 20040129 CA 2003-2493251 20030723
AU 2003254162 A1 20040209 AU 2003-254162 20030723
US 2004115815 A1 20040617 US 2003-628587 20030723
EP 1554386 A2 20050720 EP 2003-766024 20030723
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
JP 2005533504 T2 20051110 JP 2004-523400 20030723
PRIORITY APPLN. INFO.: US 2002-399040P P 20020724
WO 2003-US23239 W 20030723

AB The invention claims methods for construction of small interfering RNA (**siRNA**) expression cassettes using a polymerase **primer hairpin** linker. The expression cassette is constructed from a self-priming oligonucleotide comprising three segments (from 5' to 3' direction): (1) a 5' leader sequence between 4 and 27 nucleotides long with at least four consecutive adenylyl residues (complementary to the polIII transcription terminator) at its 3' end, (2) a coding sequence for the sense strand of an **siRNA**, preferably 11-27 nucleotides, and (3) a polymerase **primer hairpin** linker. The 5' leader sequence can include restriction site(s) for cloning **siRNA** coding sequences into expression cassettes. The polymerase **primer hairpin** linker forms a short stem-loop structure involving the 3' end of the self-priming oligonucleotide. The sequence encoding the corresponding antisense strand of the **siRNA** and the complement of the 5' leader sequence are produced by **primer** extension from the 3' end of the polymerase **primer hairpin** linker. The product of the primer extension reaction includes a stem-loop that must be denatured. Blocking primers are then annealed to the 5' and 3' ends of the denatured DNA. A complementary strand for the entire mol. is synthesized, thereby producing a duplex DNA that can be used to complete the construction of the expression cassette. The methods allow rapid construction of a single transcriptional unit encoding both strands of a hairpin **siRNA**, regardless of sequence. Expression cassettes of the invention contain an RNA polymerase III-dependent promoter and regulatory elements for inducible transcription of siRNAs. In addition, the invention includes **libraries** comprising the expression cassettes of the invention, including vectors for transforming cells, such as replication-deficient retroviral vectors. Methods of the invention and **siRNA** expression vectors may be useful for elucidation of gene function and identification of novel genes. Specifically, the present invention relates to methods and compns. for improved functional genomic screening, functional inactivation of specific essential or non-essential genes, and identification of genes that are modulated in response to specific stimuli or encode recognizable phenotypic traits. The examples of the invention describe construction of a **randomized siRNA** gene **library** under control of a U6 snRNA promoter, construction of an **siRNA** expression vector with a tetracycline-inducible promoter, and down-regulation of firefly luciferase in a breast cancer cell line (MCF7-luc) by plasmid pLPR-U6-lucB-siRNAh. Another example describes use of a hairpin **siRNA** gene **library** to enrich for siRNAs that down-regulate surface CD4 expression in the human T cell line, Molts-4.

L2 ANSWER 3 OF 4 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-450394 [42] WPIDS
CROSS REFERENCE: 2004-441179 [41]; 2004-460770 [43]
DOC. NO. CPI: C2004-168822
TITLE: Making a transcription product of a target nucleic acid sequence, for diagnosing diseases in plants or animals, comprises admixing RNA polymerase, single-stranded transcription substrate and nucleoside triphosphates .
DERWENT CLASS: B04 D16
INVENTOR(S): DAHL, G A; DAVYDOVA, E; GERDES, S; JENDRISAK, J J; ROTHMAN-DENES, L
PATENT ASSIGNEE(S): (EPIC-N) EPICENTRE TECHNOLOGIES
COUNTRY COUNT: 106
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004048594	A2	20040610	(200442)*	EN	264
RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG UZ VC VN YU ZA ZM ZW					
AU 2003294447	A1	20040618	(200471)		
EP 1585824	A2	20051019	(200568)	EN	
R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HU IE IT LI LT LU LV MC MK NL PT RO SE SI SK TR					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004048594	A2	WO 2003-US37356	20031121
AU 2003294447	A1	AU 2003-294447	20031121
EP 1585824	A2	EP 2003-789931	20031121
		WO 2003-US37356	20031121

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2003294447	A1	Based on	WO 2004048594
EP 1585824	A2	Based on	WO 2004048594

PRIORITY APPLN. INFO: US 2002-428013P 20021121
AN 2004-450394 [42] WPIDS
CR 2004-441179 [41]; 2004-460770 [43]
AB WO2004048594 A UPAB: 20051024
NOVELTY - Making a transcription product corresponding to a target nucleic acid sequence comprises admixing RNA polymerase, a single-stranded transcription substrate and nucleoside triphosphates (NTPs), and incubating the RNA polymerase and the single-stranded transcription substrate to allow synthesis of transcription product.

DETAILED DESCRIPTION - Making transcription product corresponding to a target nucleic acid sequence comprising:

(a) obtaining an RNA polymerase that can transcribe RNA using a single-stranded promoter;

(b) obtaining a single stranded DNA comprising a target nucleic sequence that is present in or complementary to at least a portion of a

target nucleic acid in a sample;

(c) obtaining a single-stranded transcription substrate by operably joining to the single-stranded DNA a single-stranded polynucleotide comprising a promoter sequence that binds the RNA polymerase;

(d) obtaining NTPs that are substrates for the RNA polymerase and that are complementary to canonical nucleic acid bases;

(e) admixing the RNA polymerase, single-stranded transcription substrate and NTPs; and

(f) incubating the RNA polymerase and the single-stranded transcription substrate to allow synthesis of transcription product.

INDEPENDENT CLAIMS are also included for the following:

(1) obtaining additional rounds of synthesis of transcription product corresponding to a target nucleic acid sequence;

(2) attenuating expression of a target gene in a cell;

(3) a hairpin RNA made by the method above;

(4) a cell comprising the hairpin RNA;

(5) a kit for performing the method above (or for making the **hairpin** above), the kit comprising an RNA polymerase defined above and a promoter splice template oligo, promoter ligation oligo or promoter **primer** (or an oligonucleotide comprising a sequence corresponding to a single-stranded promoter sequence);

(6) cloning a target nucleic acid;

(7) constructing a nucleic acid **library** comprising clones of substantially all nucleic acids or all mRNAs within a sample by using the method of (6);

(8) a composition comprising a clone made by the method of (6) or a nucleic acid **library** made by using the method of (7);

(9) a host cell comprising a circular DNA molecule made by using the method of (6);

(10) a circular DNA molecule made by using the method of (6);

(11) a kit for performing the method of (6); and

(12) detecting an analyte in a sample.

USE - The method is useful for making transcription product (e.g., hairpin RNA) corresponding to a target nucleic acid sequence (claimed) to detect target nucleic acids in living cells. The method is useful for research, diagnostic and therapeutic applications, such as preparing cDNA corresponding to full-length mRNA, making sense or anti-sense probes, detecting gene- or organism-specific sequences, cloning, cell signaling, or making RNA for use in RNAi. The method is useful for diagnosing diseases in plants and animals, including humans, and for testing products such as food, blood and tissue cultures, for contaminants. The methods are useful for detecting cellular nucleic acids in whole cells from a specimen such as a fixed or paraffin-embedded section, or from microorganisms immobilized on a solid support such as replica-plated bacteria or yeast.

Dwg.0/24

L2 ANSWER 4 OF 4 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 2004-248481 [23] WPIDS

DOC. NO. CPI: C2004-097136

TITLE: Use of double stranded DNA molecules for producing double stranded RNA or hairpin RNA, for mediating RNA interference or for treating or preventing diseases resulting from expression of a target gene.

DERWENT CLASS: B04 D16

INVENTOR(S): ARNDT, G M; CAIRNS, M; LAI, A; TRAN, N

PATENT ASSIGNEE(S): (JOHJ) JOHNSON & JOHNSON RES PTY LTD

COUNTRY COUNT: 106

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004022777	A1	20040318	(200423)*	EN	75

RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS
LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK
DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR
KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO NZ OM PG PH
PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC
VN YU ZA ZM ZW

AU 2003257256 A1 20040329 (200459)

EP 1546402 A1 20050629 (200543) EN

R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HU IE IT LI LT LU LV
MC MK NL PT RO SE SI SK TR

JP 2005537015 W 20051208 (200580) 43

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004022777	A1	WO 2003-AU1142	20030904
AU 2003257256	A1	AU 2003-257256	20030904
EP 1546402	A1	EP 2003-793475	20030904
		WO 2003-AU1142	20030904
JP 2005537015	W	WO 2003-AU1142	20030904
		JP 2004-533057	20030904

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2003257256	A1	Based on	WO 2004022777
EP 1546402	A1	Based on	WO 2004022777
JP 2005537015	W	Based on	WO 2004022777

PRIORITY APPLN. INFO: AU 2003-901418 20030326; AU 2002-951224 20020904

AN 2004-248481 [23] WPIDS

AB WO2004022777 A UPAB: 20040405

NOVELTY - Use of double stranded DNA molecules in the production of double stranded RNA or hairpin RNA, for mediating RNA interference or for treating or preventing diseases resulting from expression of a target gene.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) producing a DNA molecule where mRNA transcribed from the DNA molecule forms hairpin RNA (hRNA);

(2) preparing an expression vector, where its expression produces double stranded RNA (dsRNA);

(3) determining a function of a gene;

(4) an expression vector for use in suppressing expression of a target gene, the vector comprising a pair of convergent promoters and a DNA molecule positioned between, where the DNA molecule comprises a target-specific sequence flanked by two directional transcription terminators, the target-specific sequence comprising a sequence of at least 14 nucleotides having at least 90% identity to a segment of the target gene; and

(5) inhibiting expression of a target gene in a cell.

ACTIVITY - Immunosuppressive; Cytostatic; Antimicrobial.

MECHANISM OF ACTION - Gene Therapy.

USE - The double stranded DNA molecules are useful in the production of double stranded RNA or hairpin RNA, for mediating RNA interference or for treating or preventing diseases resulting from expression of a target gene. The compositions are useful in treating or preventing diseases resulting from expression of a target gene. Diseases include autoimmune

diseases, cancer, infection by a pathogen or over-expression of the target gene.
Dwg.0/18

=> librar? and random? and (hairpin (s) primer)
L3 13 LIBRAR? AND RANDOM? AND (HAIRPIN (S) PRIMER)

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4 11 DUP REM L3 (2 DUPLICATES REMOVED)

=> d his

(FILE 'HOME' ENTERED AT 19:01:58 ON 06 JUN 2006)

FILE 'MEDLINE, BIOSIS, CAPLUS, SCISEARCH, EMBASE, WPIDS' ENTERED AT 19:02:22 ON 06 JUN 2006
L1 5 SIRNA AND LIBRAR? AND RANDOM? AND (HAIRPIN (S) PRIMER)
L2 4 DUP REM L1 (1 DUPLICATE REMOVED)
L3 13 LIBRAR? AND RANDOM? AND (HAIRPIN (S) PRIMER)
L4 11 DUP REM L3 (2 DUPLICATES REMOVED)

=> l3 not l2
L5 9 L3 NOT L2

=> d ibib abs l5 1-9

L5 ANSWER 1 OF 9 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:472598 CAPLUS
DOCUMENT NUMBER: 139:48115
TITLE: DNA amplification and sequencing of DNA molecules generated by **random** fragmentation by tailing with a universal primer
INVENTOR(S): Makarov, Vladimir L.; Sleptsova, Irina; Kamberov, Emmanuel; Bruening, Eric
PATENT ASSIGNEE(S): Rubicon Genomics Inc., USA
SOURCE: PCT Int. Appl., 120 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003050242	A2	20030619	WO 2002-US37322	20021113
WO 2003050242	A3	20031023		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2002359436	A1	20030623	AU 2002-359436	20021113
US 2003143599	A1	20030731	US 2002-293048	20021113
EP 1451365	A2	20040901	EP 2002-793975	20021113
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,				

IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK
JP 2005535283 T2 20051124 JP 2003-551264 20021113
PRIORITY APPLN. INFO.: US 2001-338224P P 20011113
WO 2002-US37322 W 20021113

AB Methods of preparing DNA **libraries**, e.g. for sequencing, using DNA prepared by **random** fragmentation using amplification with a universal primer are described. In some embodiments, the present invention regards preparing a template for DNA sequencing by **random** fragmentation. The DNA may be **randomly** fragmented by chemical, enzymic, or mech. methods. The fragments then have a common sequence (a universal sequence) added to their 3'-termini, such as by ligation of an adaptor sequence or by homopolymeric tailing with terminal deoxynucleotidyltransferase. The sequences may then be selectively amplified for further processing using the universal sequence as one of a primer pair with a second primer for an area of interest, such as a sequence identified during sequencing.

L5 ANSWER 2 OF 9 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2005-403349 [41] WPIDS
CROSS REFERENCE: 2005-261639 [27]; 2005-261640 [27]; 2005-294733 [30]
DOC. NO. NON-CPI: N2005-327142
DOC. NO. CPI: C2005-124625
TITLE: Detecting a nucleic acid target in a sample by combining with the sample a circular nucleic acid probe, useful in amplifying nucleic acids for detection and cloning.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): WANG, Y; ZONG, Y
PATENT ASSIGNEE(S): (WANG-I) WANG Y; (ZONG-I) ZONG Y
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2005112639	A1	20050526	(200541)*		33

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2005112639	A1 Provisional	US 2003-506218P	20030926
		US 2004-952046	20040927

PRIORITY APPLN. INFO: US 2003-506218P 20030926; US 2004-952046 20040927
AN 2005-403349 [41] WPIDS
CR 2005-261639 [27]; 2005-261640 [27]; 2005-294733 [30]
AB US2005112639 A UPAB: 20050629
NOVELTY - Detecting a nucleic acid target in a sample comprises combining with the sample a circular nucleic acid probe, where a first portion of the probe hybridizes with a first portion of the target, generating a free 3' end in the target, synthesizing from the free 3' end a new nucleic acid complementary to a second portion of the probe by rolling circle amplification, and detecting the new nucleic acid as an indication of the target.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) making RNA comprising combining with a sample comprising a nucleic acid target a circular nucleic acid probe comprising an RNA polymerase promoter, under conditions wherein a first portion of the probe hybridizes with a first portion of the target, generating a free 3' end in the first portion of the target, synthesizing from the free 3' end a DNA complementary to a second portion of the probe and comprising the promoter

by rolling circle amplification, and transcribing the DNA from the promoter using an RNA polymerase to make RNA; and

(2) amplifying a polynucleotide, comprising forming a linear polynucleotide having 3' and 5' hairpins, ligating 3' and 5' ends of the linear target to form a circularized polynucleotide, and amplifying the circularized polynucleotide by rolling circle amplification.

USE - The methods and compositions of the present invention are useful in amplifying nucleic acids for detection and cloning by rolling circle amplification.

Dwg.0/16

L5 ANSWER 3 OF 9 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 2005-261640 [27] WPIDS
CROSS REFERENCE: 2005-261639 [27]; 2005-294733 [30]; 2005-403349 [41]
DOC. NO. CPI: C2005-082749
TITLE: Amplifying polynucleotide, involves ligating 3' and 5' terminals of linear polynucleotide to form circularized polynucleotide and amplifying circularized polynucleotide by rolling circle amplification.
DERWENT CLASS: B04 D16
INVENTOR(S): WANG, Y; ZONG, Y
PATENT ASSIGNEE(S): (WANG-I) WANG Y; (ZONG-I) ZONG Y
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2005069939	A1	20050331	(200527)*		22

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2005069939	A1 Provisional	US 2003-506218P	20030926
		US 2004-952076	20040927

PRIORITY APPLN. INFO: US 2003-506218P 20030926; US 2004-952076 20040927

AN 2005-261640 [27] WPIDS
CR 2005-261639 [27]; 2005-294733 [30]; 2005-403349 [41]
AB US2005069939 A UPAB: 20050629

NOVELTY - Amplifying (M1) a polynucleotide comprising forming a linear polynucleotide having 3' and 5' hairpins, ligating 3' and 5' terminals of the linear target to form a circularized polynucleotide, and amplifying the circularized polynucleotide by rolling circle amplification, is new.

USE - (M1) is useful for amplifying a polynucleotide (e.g. DNA or linear nucleic acid target), or producing circular copy DNA, which involves hybridizing a first **primer** to a 3' portion of a template region of a target strand, polymerizing from the **primer** a first copy DNA of the template region, displacing from the template region the first copy DNA, forming a **hairpin** second **primer** at a 3' portion of the first copy DNA, polymerizing from the **hairpin primer** a second copy DNA of a portion of the first copy DNA, and ligating the 5' terminal of the first copy DNA with the 3' terminal of the second copy DNA to form a circular copy DNA. The displacing step is effected with nuclease, base or strand displacement (claimed).

DESCRIPTION OF DRAWING(S) - The figure shows the steps involved in amplifying DNA by rolling circle amplification.

Dwg.4/5

L5 ANSWER 4 OF 9 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2005-261639 [27] WPIDS
CROSS REFERENCE: 2005-261640 [27]; 2005-294733 [30]; 2005-403349 [41]
DOC. NO. CPI: C2005-082748
TITLE: Detecting nucleic acid target in sample, by combining with sample circular nucleic acid probe, generating free 3' end, synthesizing new nucleic acid by rolling circle amplification and detecting nucleic acid as indication of target.
DERWENT CLASS: B04 D16
INVENTOR(S): WANG, Y; ZONG, Y
PATENT ASSIGNEE(S): (WANG-I) WANG Y; (ZONG-I) ZONG Y; (FULL-N) FULL MOON BIOSYSTEMS INC
COUNTRY COUNT: 108
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2005069938	A1	20050331	(200527)*		22
WO 2005030983	A2	20050407	(200527)	EN	

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NA NL OA PL PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2005069938	A1 Provisional	US 2003-506218P	20030926
		US 2004-952026	20040927
WO 2005030983	A2	WO 2004-US31652	20040927

PRIORITY APPLN. INFO: US 2003-506218P 20030926; US 2004-952026 20040927
AN 2005-261639 [27] WPIDS
CR 2005-261640 [27]; 2005-294733 [30]; 2005-403349 [41]
AB US2005069938 A UPAB: 20050629
NOVELTY - Detecting (M1) a nucleic acid target in a sample comprising combining a circular nucleic acid probe with a sample, so that first portion of the probe hybridizes with first portion of the target, generating a free 3' end in the first portion of the target, synthesizing a new nucleic acid complementary to second portion of the probe by rolling circle amplification and detecting new nucleic acid as an indication of the target, is new.

DETAILED DESCRIPTION - Detecting (M1) a nucleic acid target in a sample, involves combining with sample a circular nucleic acid probe, under conditions where a first portion of the probe hybridizes with a first portion of the target, generating a free 3' end in the first portion of the target, combining with the sample a circular nucleic acid probe, under conditions where a first portion of the probe hybridizes with a first portion of the fragment, synthesizing from the free 3' end a new nucleic acid complementary to a second portion of the probe by rolling circle amplification, and detecting the new nucleic acid as an indication of the target.

INDEPENDENT CLAIMS are also included for:
(1) making (M2) RNA comprising:
(a) combining with a sample comprising a nucleic acid target a

circular nucleic acid probe comprising an RNA polymerase promoter, under conditions where a first portion of the probe hybridizes with a first portion of the target, generating a free 3' end in the first portion of the target, synthesizing from the free 3' end a DNA complementary a second portion of the probe and comprising the promoter by rolling circle amplification and transcribing the DNA from the promoter using an RNA polymerase to make RNA; or

(b) combining with a sample comprising a nucleic acid target a nucleic acid fragment, where a first portion of the fragment hybridizes to a first portion of the target, generating a free 3' end in the fragment, contacting the target-hybridized fragment with a circular nucleic acid probe comprising an RNA polymerase promoter sequence, under conditions where a first portion of the probe hybridizes with a second portion of the fragment, synthesizing from the free 3' end a DNA complementary to a second portion of the probe and comprising the promoter by rolling circle amplification and transcribing the DNA from the promoter using RNA polymerase to make RNA; and

(2) amplifying a polynucleotide comprising a forming a linear polynucleotide having 3' and 5' hairpins, ligating 3' and 5' ends of the linear target to form a circularized polynucleotide and amplifying the circularized polynucleotide by rolling circle amplification.

USE - (M1) is useful for detecting a nucleic acid target such as mRNA, rRNA, interfering RNA (RNAi), heteronuclear RNA, genomic DNA or cDNA, in a sample (claimed). (M1) is useful for detecting mutations.

ADVANTAGE - (M1) allows cloning of full-length target nucleic acid sequences and amplification and cloning of entire genomes if desired. (M1) enables detection without ligation and few or no externally supplied primers for amplification, thus simplifying the overall reactions. (M1) can be performed in multiplexed reaction (simultaneous detection or two or more nucleic acids in a single sample).

DESCRIPTION OF DRAWING(S) - The figure shows an overview of method for detecting RNA and DNA with circular probes.

Dwg.5/5

L5 ANSWER 5 OF 9 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 2004-534375 [51] WPIDS
DOC. NO. CPI: C2004-196634
TITLE: Use of interfering RNA for decreasing the level of a target mRNA in a host cell, selecting a double-stranded RNA molecule, or constructing a **library** of RNA hairpin molecules.
DERWENT CLASS: B04 D16
INVENTOR(S): JAYASENA, S; KHVOROVA, A; REYNOLDS, A
PATENT ASSIGNEE(S): (AMGE-N) AMGEN INC; (JAYA-I) JAYASENA S; (KHVO-I) KHVOROVA A; (REYN-I) REYNOLDS A
COUNTRY COUNT: 108
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004061083	A2	20040722	(200451)*	EN	204
RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG UZ VC VN YU ZA ZM ZW					
AU 2003299970	A1	20040729	(200477)		
US 2004248299	A1	20041209	(200481)		
EP 1575980	A2	20050921	(200562)	EN	
R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HU IE IT LI LT LU LV					

MC MK NL PT RO SE SI SK TR

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004061083	A2	WO 2003-US41377	20031224
AU 2003299970	A1	AU 2003-299970	20031224
US 2004248299	A1 Provisional	US 2002-436849P	20021227
		US 2003-745395	20031222
EP 1575980	A2	EP 2003-800235	20031224
		WO 2003-US41377	20031224

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2003299970	A1 Based on	WO 2004061083
EP 1575980	A2 Based on	WO 2004061083

PRIORITY APPLN. INFO: US 2002-436849P 20021227; US 2003-745395 20031222

AN 2004-534375 [51] WPIDS

AB WO2004061083 A UPAB: 20040810

NOVELTY - Use of interfering RNA for decreasing the level of a target mRNA in a host cell, selecting a double-stranded RNA molecule, or constructing a **library** of RNA hairpin molecules.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:

(1) decreasing the level of a target mRNA in a host cell;

(2) selecting a double-stranded RNA molecule;

(3) constructing a **library** of RNA hairpin molecules;

(4) identifying a target gene; and

(5) a **library** comprising RNA hairpin molecules, where each hairpin molecule comprises a first region, a second region, and a third region, where the first region comprises a **random** nucleotide sequence having 5-500 nucleotides and the third region comprises a nucleotide sequence that is substantially complementary to at least a portion of the first region.

USE - The interfering RNA is useful for decreasing the level of a target mRNA in a host cell, selecting a double-stranded RNA molecule, or constructing a **library** of RNA hairpin molecules.

Dwg.0/50

L5 ANSWER 6 OF 9 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 2004-123391 [12] WPIDS

DOC. NO. CPI: C2004-049783

TITLE: New DNA expression cassette comprising a partially **randomized** DNA sequence, useful for elucidation of gene function and identification of novel genes.

DERWENT CLASS: B04 D16

INVENTOR(S): CHATTERTON, J E; KE, N; LI, H; RHOADES, K L; WONG-STAAL, F

PATENT ASSIGNEE(S): (IMMU-N) IMMUSOL INC

COUNTRY COUNT: 106

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004009796	A2	20040129	(200412)*	EN	73

RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK
DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR
KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO NZ OM PG PH
PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC
VN YU ZA ZM ZW

US 2004115815 A1 20040617 (200440)
AU 2003254162 A1 20040209 (200450)
EP 1554386 A2 20050720 (200547) EN
R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HU IE IT LI LT LU LV
MC MK NL PT RO SE SI SK TR
JP 2005533504 W 20051110 (200574) 46

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004009796	A2	WO 2003-US23239	20030723
US 2004115815	A1 Provisional	US 2002-399040P	20020724
		US 2003-628587	20030723
AU 2003254162	A1	AU 2003-254162	20030723
EP 1554386	A2	EP 2003-766024	20030723
		WO 2003-US23239	20030723
JP 2005533504	W	WO 2003-US23239	20030723
		JP 2004-523400	20030723

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2003254162	A1 Based on	WO 2004009796
EP 1554386	A2 Based on	WO 2004009796
JP 2005533504	W Based on	WO 2004009796

PRIORITY APPLN. INFO: US 2002-399040P 20020724; US
2003-628587 20030723

AN 2004-123391 [12] WPIDS

AB WO2004009796 A UPAB: 20040218

NOVELTY - A DNA expression cassette, is new.

DETAILED DESCRIPTION - A DNA expression cassette comprises:

(a) a partially **randomized** nucleic acid sequence having a 5' end and a 3' end and including first and second segments where:

(i) the first segment comprises a series of 0-23 bases linked 3' to a plurality of at least four consecutive adenylyl residues linked 3' to a **randomized** nucleic acid sequence of 11-27 bases;

(ii) the second segment comprises a sequence complementary to the first segment sequence and linked to the 3' end of the first segment through its 5' end by a polymerase **primer hairpin** linker having the sequence N1nN2mN3n where N3 is complementary to N1, n is a number greater than or equal to 2, and m is a number from 1 to 40; and

(b) a pol III promoter having a TATA box, operably linked to the partially **randomized** sequence, the pol III promoter being modified to allow transcription from the promoter to begin at the first base of the **randomized** nucleic acid sequence.

INDEPENDENT CLAIMS are also included for:

(1) a self-replicating DNA comprising the DNA expression cassette;

(2) a **library** of DNA expression cassettes;

(3) producing the **library** of DNA expression cassettes for expressing dsRNA having **randomized** sequences; and

(4) correlating expression of a transcription sequence for a siRNA with a phenotypic change resulting from inhibiting expression of a cellular gene by the siRNA, where expression of the cellular gene is not previously characterized as contributing to the phenotypic change.

USE - The DNA expression cassette is useful for improved functional genomic screening, functional inactivation of specific essential or non-essential genes, and identification of genes that are modulated in response to specific stimuli or encode recognizable phenotypic traits. Dwg.0/9

L5 ANSWER 7 OF 9 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-532900 [50] WPIDS
DOC. NO. CPI: C2003-144109
TITLE: Preparing a DNA molecule, useful in genomics, molecular biology and sequencing, comprises attaching a primer having substantially known sequence to at least one end of DNA fragments.
DERWENT CLASS: B04 D16
INVENTOR(S): BRUENING, E; KAMBEROV, E; MAKAROV, V L; SLEPTSOVA, I
PATENT ASSIGNEE(S): (RUBI-N) RUBICON GENOMICS INC
COUNTRY COUNT: 103
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2003050242	A2	20030619	(200350)*	EN	120
RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SC SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW					
US 2003143599	A1	20030731	(200354)		
AU 2002359436	A1	20030623	(200420)		
EP 1451365	A2	20040901	(200457)	EN	
R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI SK TR					
JP 2005535283	W	20051124	(200581)		82
AU 2002359436	A8	20051020	(200615)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003050242	A2	WO 2002-US37322	20021113
US 2003143599	A1 Provisional	US 2001-338224P	20011113
		US 2002-293048	20021113
AU 2002359436	A1	AU 2002-359436	20021113
EP 1451365	A2	EP 2002-793975	20021113
		WO 2002-US37322	20021113
JP 2005535283	W	WO 2002-US37322	20021113
		JP 2003-551264	20021113
AU 2002359436	A8	AU 2002-359436	20021113

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002359436	A1 Based on	WO 2003050242
EP 1451365	A2 Based on	WO 2003050242
JP 2005535283	W Based on	WO 2003050242
AU 2002359436	A8 Based on	WO 2003050242

PRIORITY APPLN. INFO: US 2001-338224P 20011113; US 2002-293048 20021113

AN 2003-532900 [50] WPIDS
AB WO2003050242 A UPAB: 20030805
NOVELTY - Preparing a DNA molecule comprising obtaining a DNA molecule, **randomly** fragmenting the DNA molecule to produce DNA fragments, attaching a primer having substantially known sequence to at least one end of DNA fragments to produce primer-linked fragments, and amplifying the primer-linked fragments, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) preparing a **library** of DNA molecules comprising performing the novel method;

(2) a **library** generated by the novel method;

(3) generating a **library** of DNA templates;

(4) sequencing DNA fragments concomitantly;

(5) sequencing a consecutive overlapping series of nucleic acid sequences;

(6) conditioning a 3' end of a DNA molecule by exposing the 3' end to terminal deoxynucleotidyltransferase;

(7) providing 3' exonuclease activity to the end of a DNA molecule by introducing the terminal deoxynucleotidyltransferase to the end of the molecule;

(8) preparing a probe;

(9) a labeled probe generated from the method;

(10) a kit comprising a probe generated from the method;

(11) repairing a 3' end of at least one single stranded DNA molecule comprising providing to the 3' end a terminal deoxynucleotidyltransferase;

(12) a kit for the method in (11); and

(13) detecting a damaged DNA molecule by providing to the damaged DNA molecule by providing the damaged DNA molecule terminal deoxynucleodyltransferase and a labeled guanine ribonucleotide, and/or labeled guanine deoxyribonucleotide.

USE - The method is useful in the fields of genomics, molecular biology and sequencing for preparing DNA molecules and DNA templates for sequencing, and sequencing from **randomly** fragmented DNA molecules.

Dwg.0/28

L5 ANSWER 8 OF 9 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-021218 [02] WPIDS
DOC. NO. CPI: C2003-005375
TITLE: Selectively amplifying unknown DNA sequence, useful when analyzing single nucleotide polymorphism, by digesting DNA into fragments with single-strand cohesive ends, ligating fragments with a hairpin loop adapter and amplifying the fragments.
DERWENT CLASS: B04 D16
INVENTOR(S): JEON, J; JOUNG, I; PARK, H; RHEE, J; SONG, S; WEON, S; JUN, J T; JUNG, I S; LEE, J W; PARK, H O; SONG, S N; WON, S Y
PATENT ASSIGNEE(S): (BION-N) BIONEER CORP; (BION-N) BIONIA JH; (JEON-I) JEON J; (JOUN-I) JOUNG I; (PARK-I) PARK H O; (RHEE-I) RHEE J; (SONG-I) SONG S; (WEON-I) WEON S
COUNTRY COUNT: 30
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 1256630	A2	20021113	(200302)*	EN	10
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
US 2002192769	A1	20021219	(200315)#		
CA 2344599	A1	20021107	(200316)#	EN	

JP 2003009864 A 20030114 (200316) 6
KR 2002085727 A 20021116 (200320)
US 6849404 B2 20050201 (200511)#

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 1256630	A2	EP 2002-10053	20020506
US 2002192769	A1	US 2001-849597	20010507
CA 2344599	A1	CA 2001-2344599	20010507
JP 2003009864	A	JP 2002-131307	20020507
KR 2002085727	A	KR 2001-25637	20010507
US 6849404	B2	US 2001-849597	20010507

PRIORITY APPLN. INFO: KR 2001-25637 20010507; US 2001-849597 20010507; CA 2001-2344599 20010507

AN 2003-021218 [02] WPIDS

AB EP 1256630 A UPAB: 20050316

NOVELTY - A process for selective amplifying DNA of which base sequence is completely unknown, comprising digesting DNA into fragments having a single-strand cohesive end group, ligating the DNA fragments with a **hairpin** loop adapter having a single-strand cohesive end which can be complementarily combined and ligated on both ends of the DNA, and amplifying the fragments using DNA polymerase and **primer**.

DETAILED DESCRIPTION - A process (M1) for selective amplifying DNA of which base sequence is completely unknown, comprising:

(a) a step for digesting DNA into fragments which has a single-strand cohesive end group by using restriction enzyme, and separately from the above step, a step for preparing hairpin loop adaptor which has the single-strand cohesive end which can be complementarily combined and ligated on the both ends of the DNA fragments obtained in the above;

(b) a step for ligating the DNA fragments with the hairpin loop adapter thus prepared by using DNA ligase;

(c) a step for removing DNA fragments and hairpin loop adapter which have not participated in the ligation reaction by using exonuclease; and

(d) a step for amplifying the DNA fragment by using DNA polymerase and primer which can combine complementarily on the residual sequence from the adapter.

INDEPENDENT CLAIMS are included for the following:

(1) a process for making **library** of DNA fragment of which terminal sequence are known by using DNA of which base sequence is completely unknown, comprising:

(a) a step for digesting DNA into fragments which have single-strand cohesive end by using restriction enzyme, and separately from the above, for preparing a series of hairpin loop adapters which have single-strand cohesive end of which base sequence is known;

(b) a step for ligating the DNA fragments with the hairpin loop adapters prepared in the above step (a) by using DNA ligase; and

(c) a step for eliminating the hairpin loop only from the DNA fragments which contain hairpin loop adapter, obtained in step (b) by treating alkaline solution, RNase of single strand specific exonuclease; and

(2) a series of hairpin loop adapters which have single-strand cohesive ends, where the single-strand cohesive ends are composed of all sorts of single-strand DNA which can be made by **random** combination of four nucleotides.

USE - The process is useful for analyzing single nucleotide polymorphism in the nucleotide sequences of each individual.

Dwg.0/4

L5 ANSWER 9 OF 9 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2000-611449 [58] WPIDS
CROSS REFERENCE: 1999-287950 [24]; 2001-557931 [62]
DOC. NO. CPI: C2000-182935
TITLE: Making immobilized nucleic acid molecule array comprises creating array nucleic acid capture activity spots to which an excess of nucleic acid molecules with excluded volume greater than spots are contacted.
DERWENT CLASS: A89 B04 D16
INVENTOR(S): CHURCH, G M; MITRA, R D; MITRA, R
PATENT ASSIGNEE(S): (HARD) HARVARD COLLEGE
COUNTRY COUNT: 23
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000053812	A2	20000914	(200058)*	EN	117
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: AU CA JP					
AU 2000038761	A	20000928	(200067)		
EP 1235929	A2	20020904	(200266)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
US 6485944	B1	20021126	(200281)		
EP 1291354	A2	20030312	(200320)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
CA 2411514	A1	20000914	(200329)	EN	
JP 2003526331	W	20030909	(200360)		135
AU 2002301870	A1	20030313	(200433)#		
AU 2005201991	A1	20050602	(200541)#		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2000053812	A2		WO 2000-US6390	20000310
AU 2000038761	A		AU 2000-38761	20000310
EP 1235929	A2		EP 2000-917853	20000310
			WO 2000-US6390	20000310
US 6485944	B1	Provisional	US 1997-61511P	19971010
		Provisional	US 1998-76570P	19980302
		CIP of	US 1998-143014	19980828
			US 1999-267496	19990312
EP 1291354	A2	Div ex	EP 2000-917853	20000310
			EP 2002-79758	20000310
CA 2411514	A1	Div ex	CA 2000-2370535	20000310
			CA 2000-2411514	20000310
JP 2003526331	W		JP 2000-603433	20000310
			WO 2000-US6390	20000310
AU 2002301870	A1	Div ex	AU 2000-38761	20000310
			AU 2002-301870	20021107
AU 2005201991	A1	Div ex	AU 2000-38761	20000310
			AU 2005-201991	20050511

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000038761	A	Based on	WO 2000053812
EP 1235929	A2	Based on	WO 2000053812
EP 1291354	A2	Div ex	EP 1235929
JP 2003526331	W	Based on	WO 2000053812

PRIORITY APPLN. INFO: US 1999-267496 19990312; US
1997-61511P 19971010; US
1998-76570P 19980302; US
1998-143014 19980828; AU
2002-301870 20021107; AU
2005-201991 20050511
AN 2000-611449 [58] WPIDS
CR 1999-287950 [24]; 2001-557931 [62]
AB WO 200053812 A UPAB: 20050629
NOVELTY - Making (M1) immobilized nucleic acid molecule array (N) comprises creating array of spots of nucleic acid capture activity (I) contacting (I) with excess of (N) with an excluded column diameter greater than the diameter of the spots of (I), resulting in (N), in which each spot of (I) can bind only (N) with excluded volume diameter greater than size of spots of (I).

DETAILED DESCRIPTION - The spots of the capture activity are separated by a distance greater than diameter of the spots and size of the spots is less than the diameter of the excluded volume of nucleic acid molecule to be captured.

INDEPENDENT CLAIMS are also included for the following:

(1) detecting (M2) a nucleic acid on (N) comprising generating multiple (N) in which the nucleic acid molecules of each unit of (N) occupy positions which corresponds to those positions occupied by the nucleic acid molecules of each unit of the multiple (N) array and then subjecting one or more units of the multiple (N) (but at least one less than the total number of the multiple (N)) to a method of signal detection which involves a signal amplification method that renders each member of the multiple nucleic acid array non-reusable;

(2) preserving (M3) the resolution of nucleic acid features on a first immobilized array during cycles of array replication involves amplifying the features of a first array to yield an array of features with a hemisphere radius (r) and a cross-sectional area (q) at the surface supporting the array, such that the features remain essential distinct;

(3) making (M4) multiple (N) comprising:

(a) providing a first liquid mixture of template nucleic acid, one oligonucleotide primer, which includes a linker moiety, and monomers capable of forming a polymerized gel matrix;

(b) contacting the mixture with a solid support;

(c) forming a first layer of a polymerized gel matrix with the linker moiety covalently bound to it;

(d) providing a second liquid mixture of one oligonucleotide primer and monomers capable of forming a polymerized gel matrix;

(e) contacting the first layer with the second liquid matrix;

(f) forming a second layer of a polymerized gel matrix;

(g) amplifying the template nucleic acid and transferring amplified nucleic acid to the second layer;

(h) removing the second layer; and

(i) optionally repeating steps (c) - (g);

(4) determining (M5) the nucleotide sequence of an immobilized nucleic acid array comprising:

(a) ligating a first double-stranded nucleic acid probe having a restriction endonuclease recognition site which is separate from the cleavage site, to one end of a nucleic acid of the array;

(b) identifying one or more nucleotides at the end of the polynucleotide by the identity of the first double stranded nucleic acid probe ligated to it or by extending a strand of the polynucleotide or probe;

(c) amplifying the features of the array using a primer complementary to the first double stranded nucleic acid probe, such that only molecules which have been successfully ligated with the first double stranded nucleic acid probe are amplified;

(d) contacting the amplified array with support such that a subset of nucleic acid molecules produced by the amplifying are transferred to the support;

(e) covalently attaching the subset of nucleic acid molecules transferred in the above step to the support to form a replica of the amplified array;

(f) cleaving the nucleic acid features of the array with a nuclease recognizing the nuclease recognition site of the probe such that the nucleic acid of the features is shortened by one or more nucleotides; and

(g) repeating steps (a) - (f) until the nucleotide sequences of the features of the array are determined;

(5) a method (M6) of determining the nucleotide sequence of the features of (N) comprising:

(a) adding a mixture comprising an oligonucleotide primer and a template-dependent polymerase to an array of immobilized nucleic acid features;

(b) adding a single, fluorescently labeled deoxynucleoside triphosphate to the mixture;

(c) detecting incorporated label by monitoring fluorescence;

(d) repeating steps (b) and (c) with each of the remaining three labeled deoxynucleoside triphosphates in turn; and

(e) repeating steps (b) - (d) until the nucleotide sequence is determined;

(6) a method (M7) of determining the nucleotide sequence of the features of micro-array of nucleic acid comprising:

(a) creating a micro-array of nucleic acid features in a linear arrangement within and along one side of a polyacrylamide gel, the gel further comprising one or more oligonucleotide primers and a template-dependent polymerizing activity;

(b) amplifying the micro-array of (a);

(c) adding a mixture of deoxynucleoside triphosphates, comprising:

(i) each of the four deoxynucleoside triphosphates; and

(ii) chain-terminating analogs of each of the deoxynucleoside triphosphates labeled with a spectrally distinguishable fluorescent moiety;

(d) incubating the mixture with the micro-array;

(e) electrophoretically separating the products of the extension within the polyacrylamide gel; and

(f) determining the nucleotide sequence of the features of the micro-array by detecting the fluorescence of the extended, terminated and separated reaction products within the gel; and

(7) a method (M8) for simultaneously amplifying multiple nucleic acids comprising:

(a) creating a micro-array of immobilized oligonucleotide primers;

(b) incubating the micro-array of step (a) with amplification template and a non-immobilized oligonucleotide primer;

(c) incubating the hybridized primers and template with a DNA polymerase and deoxynucleotide triphosphates; and

(d) repeating steps (b) and (c) for a defined number of cycles to yield multiple amplified DNA molecules.

USE - For nucleic acid replication or amplification, genomic characterization, gene expression studies, medical diagnostics e.g. expression analysis and genetic polymorphism detection. They are also of use in DNA/protein binding assays and more general protein array binding assays. The methods are also useful for determining the sequences of nucleic acid on arrays.

ADVANTAGE - By using the novel nucleic acid arrays a full genome including unknown DNA sequences can be replicated. The size of the nucleic acid fragments or primers to be replicated can be from about 25-mer to about 9000-mer. The method is also quick and cost effective. The thickness of the chip is 3000 nm which provides a much higher sensitivity. The chips are compatible with inexpensive in situ polymerase chain

reaction (PCR) devices, and can be reused as many as 100 times.
Dwg.0/10

=> librar? and (hairpin (s) primer)
L6 43 LIBRAR? AND (HAIRPIN (S) PRIMER)

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7 28 DUP REM L6 (15 DUPLICATES REMOVED)

=> d his

(FILE 'HOME' ENTERED AT 19:01:58 ON 06 JUN 2006)

FILE 'MEDLINE, BIOSIS, CAPLUS, SCISEARCH, EMBASE, WPIDS' ENTERED AT 19:02:22 ON 06 JUN 2006
L1 5 SIRNA AND LIBRAR? AND RANDOM? AND (HAIRPIN (S) PRIMER)
L2 4 DUP REM L1 (1 DUPLICATE REMOVED)
L3 13 LIBRAR? AND RANDOM? AND (HAIRPIN (S) PRIMER)
L4 11 DUP REM L3 (2 DUPLICATES REMOVED)
L5 9 L3 NOT L2
L6 43 LIBRAR? AND (HAIRPIN (S) PRIMER)
L7 28 DUP REM L6 (15 DUPLICATES REMOVED)

=> l7 not l3
L8 17 L7 NOT L3

=> l8 not l2
L9 17 L8 NOT L2

=> t ti l9 1-17

L9 ANSWER 1 OF 17 MEDLINE on STN
TI Directed evolution and identification of control regions of ColE1 plasmid replication origins using only nucleotide deletions.

L9 ANSWER 2 OF 17 MEDLINE on STN
TI Hairpin ribozyme specificity in vivo: a case of promiscuous cleavage.

L9 ANSWER 3 OF 17 MEDLINE on STN
TI Cloning and characterization of two groESL operons of Rhodobacter sphaeroides: transcriptional regulation of the heat-induced groESL operon.

L9 ANSWER 4 OF 17 MEDLINE on STN
TI A simple and very efficient method for generating cDNA **libraries**
.

L9 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
TI SNP analysis using restriction digestion products amplified by nick translation and adapter/primer selection

L9 ANSWER 6 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
TI Nested oligonucleotides containing **hairpin** structures for single **primer** amplification of sequences for antibody **library** generation

L9 ANSWER 7 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
TI Methods of preparing DNA-protein fusions by covalently tagging protein with their encoding DNA

L9 ANSWER 8 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

TI Synthesizing copy of nucleic acid target, by annealing chimeric primer or chimeric nucleic acid construct that is complementary to target, with target, extending primer/nucleic acid construct using nucleic acid target as template.

L9 ANSWER 9 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI Determining the sequence of a target nucleic acid molecule, e.g. DNA molecule, comprises contacting the molecules with ligation cassettes comprising labeled oligonucleotide.

L9 ANSWER 10 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI New oligomeric compound that can hybridize with or sterically interfere with nucleic acid molecules comprising or encoding small non-coding RNA targets, useful for treating e.g., cancer and diabetes.

L9 ANSWER 11 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI Synthesizing bifunctional complex useful for generating **library** of different bifunctional complexes having encoded molecules and identifier polynucleotides identifying chemical entities participated in synthesis of encoded molecule.

L9 ANSWER 12 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI Producing a second-generation **library** of molecules with improved desired property using an initial **library** with a plurality of encoded molecules associated with an identifier nucleic acid sequence.

L9 ANSWER 13 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI New naked nucleic acid-virion protein display complex useful in functional genomics, proteomics and in protein identification for the exploration of therapeutic drugs and new diagnostic procedures.

L9 ANSWER 14 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI Selecting adenylate uridylate-rich element (ARE) coding sequences from databases, comprises extracting nucleic acids with protein coding sequences upstream, contiguous with a 3' untranslated region having a specific ARE sequence.

L9 ANSWER 15 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI Parallel sequencing of several nucleic acids, useful e.g. in gene expression analysis, using irreversibly immobilized amplification primers.

L9 ANSWER 16 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI 5' nuclease amplification assay using fluorescence-quencher probes for determination of a genotype at multiple allelic sites.

L9 ANSWER 17 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI Nucleic acid amplification, detection and synthesis methods - using primer-promoter complex, where primer is responsible for synthesis of 1st and 2nd strands, the transcription of which is initiated by promoter.

=> d ibib abs 19 1-17

L9 ANSWER 1 OF 17 MEDLINE on STN
ACCESSION NUMBER: 2005420568 MEDLINE
DOCUMENT NUMBER: PubMed ID: 16051272
TITLE: Directed evolution and identification of control regions of ColE1 plasmid replication origins using only nucleotide deletions.
AUTHOR: Kim Dewey; Rhee Yoon; Rhodes Denise; Sharma Vikram; Sorenson Olav; Greener Alan; Smider Vaughn
CORPORATE SOURCE: IntegriGen, Inc., 42 Digital Dr. Bldg. 6, Novato, CA 94949,

USA.
SOURCE: Journal of molecular biology, (2005 Aug 26) Vol. 351, No. 4, pp. 763-75.
Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200509
ENTRY DATE: Entered STN: 9 Aug 2005
Last Updated on STN: 21 Sep 2005
Entered Medline: 20 Sep 2005

AB Genes can be mutated by altering DNA content (base changes) or DNA length (insertions or deletions). Most in vitro directed evolution processes utilize nucleotide content changes to produce DNA **libraries**. We tested whether gain of function mutations could be identified using a mutagenic process that produced only nucleotide deletions. Short nucleotide stretches were deleted in a plasmid encoding lacZ, and screened for increased beta-galactosidase activity. Several mutations were found in the origin of replication that quantitatively and qualitatively altered plasmid behavior in vivo. Some mutations allowed co-residence of ColE1 plasmids in Escherichia coli, and implicate **hairpin** structures II and III of the ColE1 RNA **primer** as determinants of plasmid compatibility. Thus, useful and unexpected mutations can be found from **libraries** containing only deletions.

L9 ANSWER 2 OF 17 MEDLINE on STN
ACCESSION NUMBER: 1999216284 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10198217
TITLE: Hairpin ribozyme specificity in vivo: a case of promiscuous cleavage.
AUTHOR: Denman R B
CORPORATE SOURCE: Laboratory of Molecular Neurobiology, Department of Molecular Biology, New York State Institute for Basic Research in Developmental Disabilities, 1050 Forest Hill Road, Staten Island, New York, 10314, USA..
bob1028@interport.net
CONTRACT NUMBER: AG 04220-10A2 (NIA)
SOURCE: Biochemical and biophysical research communications, (1999 Apr 13) Vol. 257, No. 2, pp. 356-60.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 7 Jun 1999
Last Updated on STN: 7 Jun 1999
Entered Medline: 24 May 1999

AB We have used differential display to address the question of ribozyme specificity in vivo. Stably transfected PC12 cells bearing either a **hairpin** ribozyme expression plasmid targeted to betaAPP mRNA or the vector alone were analyzed using nine different **primer** pairs. One of the few differentially expressed genes obtained from this screen corresponded to rat ribosomal protein L19. Steady-state levels of L19 mRNA were lower in ribozyme-transfected cells compared to either vector-transfected cells or native PC12 cells, and a sequence within the L19 message was cleaved by the betaAPP hairpin ribozyme in vitro. These data imply that sequence-specific unintended cleavage of non-target mRNAs may present a formidable problem to the use of hairpin ribozyme therapeutic agents.

L9 ANSWER 3 OF 17 MEDLINE on STN
ACCESSION NUMBER: 97144535 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8990302
TITLE: Cloning and characterization of two groESL operons of Rhodobacter sphaeroides: transcriptional regulation of the heat-induced groESL operon.
AUTHOR: Lee W T; Terlesky K C; Tabita F R
CORPORATE SOURCE: Department of Microbiology, The Ohio State University, Columbus 43210-1292, USA.
CONTRACT NUMBER: GM24497 (NIGMS)
SOURCE: Journal of bacteriology, (1997 Jan) Vol. 179, No. 2, pp. 487-95.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U37369; GENBANK-U66831
ENTRY MONTH: 199702
ENTRY DATE: Entered STN: 27 Feb 1997
Last Updated on STN: 27 Feb 1997
Entered Medline: 13 Feb 1997

AB The nonsulfur purple bacterium Rhodobacter sphaeroides was found to contain two groESL operons. The groESL1 heat shock operon was cloned from a genomic **library**, and a 2.8-kb DNA fragment was sequenced and found to contain the groES and groEL genes. The deduced amino acid sequences of GroEL1 (cpn60) and GroES1 (cpn10) were in agreement with N-terminal sequences previously obtained for the isolated proteins (K. C. Terlesky and F. R. Tabita, Biochemistry 30:8181-8186, 1991). These sequences show a high degree of similarity to groESL genes isolated from other bacteria. Northern analysis indicated that the groESL1 genes were expressed as part of a 2.2-kb polycistronic transcript that is induced 13-fold after heat shock. Transcript size was not affected by heat shock; however, the amount of transcript was induced to its greatest extent 15 to 30 min after a 40 degrees C heat shock, from an initial temperature of 28 degrees C, and remained elevated up to 120 min. The R. sphaeroides groESL1 operon contains a putative hairpin loop at the start of the transcript that is present in other bacterial heat shock genes. **Primer** extension of the message showed that the transcription start site is at the start of this conserved **hairpin** loop. In this region were also found putative -35 and -10 sequences that are conserved upstream from other bacterial heat shock genes. Transcription of the groESL1 genes was unexpectedly low under photoautotrophic growth conditions. Thus far, it has not been possible to construct a groESL1 deletion strain, perhaps indicating that these genes are essential for growth. A second operon (groESL2) was also cloned from R. sphaeroides, using a groEL1 gene fragment as a probe; however, no transcript was observed for this operon under several different growth conditions. A groESL2 deletion strain was constructed, but there was no detectable change in the phenotype of this strain compared to the parental strain.

L9 ANSWER 4 OF 17 MEDLINE on STN
ACCESSION NUMBER: 84109562 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6198242
TITLE: A simple and very efficient method for generating cDNA **libraries**.
AUTHOR: Gubler U; Hoffman B J
SOURCE: Gene, (1983 Nov) Vol. 25, No. 2-3, pp. 263-9.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M10272
ENTRY MONTH: 198403
ENTRY DATE: Entered STN: 19 Mar 1990
Last Updated on STN: 19 Mar 1990
Entered Medline: 23 Mar 1984

AB A simple method for generating cDNA **libraries** from submicrogram quantities of mRNA is described. It combines classical first-strand synthesis with the novel RNase H-DNA polymerase I-mediated second-strand synthesis [Okayama, H., and Berg, P., Mol. Cell. Biol. 2 (1982) 161-170]. Neither the elaborate vector-**primer** system nor the classical **hairpin** loop cleavage by S1 nuclease are used. cDNA thus made can be tailed and cloned without further purification or sizing. Cloning efficiencies can be as high as 10(6) recombinants generated per microgram mRNA, a considerable improvement over earlier methods. Using the fully sequenced 1300 nucleotide-long bovine preproenkephalin mRNA, we have established by sequencing that the method yields faithful full-length transcripts. This procedure considerably simplifies the establishment of cDNA **libraries** and thus the cloning of low-abundance mRNAs.

L9 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:23043 CAPLUS
DOCUMENT NUMBER: 138:67825
TITLE: SNP analysis using restriction digestion products amplified by nick translation and adapter/primer selection
INVENTOR(S): Makarov, Vladimir L.; Langmore, John P.
PATENT ASSIGNEE(S): Rubicon Genomics Inc., USA
SOURCE: PCT Int. Appl., 144 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 2003002752	A2	20030109	WO 2002-US20200		20020625
WO 2003002752	A3	20030306			
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW					
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG					
US 2004197791	A1	20041007	US 2003-481488		20031218
PRIORITY APPLN. INFO.:			US 2001-302172P	P	20010629
			WO 2002-US20200	W	20020625

AB The present invention is directed to amplification of a single nucleotide polymorphism by utilizing a **library** of nick translate mols. The methods are also directed to highly multiplexed amplification of a nucleic acid sequence to facilitate detection of a single nucleotide polymorphism. The DNA of interest is cleaved with a restriction enzyme. The cleavage products are then ligated with an adapter oligonucleotide that can serve as a starting point for nick translation. The adapters carry a single-stranded nick that is used by a DNA polymerase as a starting point for amplification. The DNA is then amplified by nick translation in combination with a primer-driven amplification such as PCR and the

amplification products passed on to a prior art method for SNP anal. The primers are derived from the adapters. Methods of selecting sequence-specific adapter-**primer** oligonucleotides from **libraries** of **hairpin** oligonucleotides are described. The adapters are ligated to the restriction fragments and hybridized with hairpin oligonucleotides that carry a 5 base extension to give sequence specificity (PENTAmers). Hybrids are captured with an immobilized probe. Extension products from the nick translation can be captured by incorporation of an affinity label substrate into the polymerase reaction. Methods of multiplexing the amplification and the anal. using different primers and reporter groups are described.

L9 ANSWER 6 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:466233 CAPLUS
DOCUMENT NUMBER: 137:58545
TITLE: Nested oligonucleotides containing **hairpin** structures for single **primer** amplification of sequences for antibody **library** generation
INVENTOR(S): Bowdish, Katherine S.; Barbas-Frederickson, Shana; Lin, Ying-Shi; Mcwhirter, John; Maruyama, Toshiaki
PATENT ASSIGNEE(S): Alexion Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 54 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 2002048401	A2	20020620	WO 2001-US47727		20011210
WO 2002048401	A3	20030912			
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW					
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG					
CA 2436693	AA	20020620	CA 2001-2436693		20011210
AU 2002030734	A5	20020624	AU 2002-30734		20011210
EP 1366191	A2	20031203	EP 2001-990978		20011210
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR					
US 2005079489	A1	20050414	US 2001-14012		20011210
US 6919189	B2	20050719			
US 2004101886	A1	20040527	US 2003-628109		20030728
PRIORITY APPLN. INFO.:			US 2000-254669P	P	20001211
			US 2001-323400P	P	20010919
			US 2001-14012	A3	20011210
			WO 2001-US47727	W	20011210

AB Templates that are engineered to contain a predetd. sequence and a hairpin structure are provided by a nested oligonucleotide extension reaction. The engineered template allows Single Primer Amplification (SPA) to amplify a target sequence within the engineered template. In particularly useful embodiments, the target sequences from the engineered templates are cloned into expression vehicles to provide a **library** a polypeptides or proteins, such as, for example, an antibody **library**. The method involves annealing a primer to a template

nucleic acid wherein the primer has a first portion that anneals to the template and a second portion of predetd. sequence. The desired polynucleotide is synthesized and the template is separated from the polynucleotide. A nested oligonucleotide is annealed to the second end of the said synthesized polynucleotide wherein the first end of the nested oligonucleotide anneals to the second end of the polynucleotide and the second portion of the nested oligonucleotide contains a hairpin structure. Thereafter, the desired polynucleotide is extended, complementary to the hairpin region of the nested oligonucleotide and a terminal portion that is complementary to the predetd. sequence. The extended polynucleotide may be amplified using a single primer with a predetd. sequence. This method may be modified to amplify a family of related nucleic acid sequences to build a complex **library** of polypeptides.

L9 ANSWER 7 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2000:384485 CAPLUS
DOCUMENT NUMBER: 133:27341
TITLE: Methods of preparing DNA-protein fusions by covalently tagging protein with their encoding DNA
INVENTOR(S): Lohse, Peter; Kurz, Markus; Wagner, Richard
PATENT ASSIGNEE(S): Phylos, Inc., USA
SOURCE: PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 2000032823	A1	20000608	WO 1999-US28472		19991202
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM					
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
CA 2350417	AA	20000608	CA 1999-2350417		19991202
EP 1137812	A1	20011004	EP 1999-967171		19991202
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO					
US 6416950	B1	20020709	US 1999-453190		19991202
JP 2002531105	T2	20020924	JP 2000-585454		19991202
NZ 511699	A	20030228	NZ 1999-511699		19991202
AU 775997	B2	20040819	AU 2000-23509		19991202
AU 2000023509	A5	20000619			
NO 2001002735	A	20010723	NO 2001-2735		20010601
US 2002177158	A1	20021128	US 2002-180819		20020626
PRIORITY APPLN. INFO.:			US 1998-110549P	P	19981202
			US 1999-453190	A3	19991202
			WO 1999-US28472	W	19991202

AB The invention provides methods for covalently tagging proteins with their encoding DNA sequences. In general, the first method involves: (a) linking a puromycin(as peptide acceptor)-bound DNA primer to an mRNA mol. at or near its 3'-end; (b) in vitro translating the mRNA to produce a protein product (10-300 amino acids long) which will be covalently bound to the DNA primer; and (c) reverse-transcribing the RNA to cDNA and produce a DNA-protein fusion. The second method involves: (a) generating RNA-protein fusion; (b) hybridizing a DNA primer to the fusion at or near

mRNA's 3'-end; and (c) reverse-transcribing the RNA to produce a DNA-protein fusion. For the second method, the mRNA may be removed by RNaseH digestion and the DNA primer can be crosslinked to puromycin after hybridization with mRNA through an oligonucleotide already bound to puromycin or through a photocrosslinking agent such as psoralen. These DNA-protein fusions (chemical more stable than RNA-protein fusion) may be used in mol. evolution and recognition techniques for various therapeutic, diagnostic, or research purposes, such as: selection of the desired protein or screening for desired cDNA in the combinatory **library** or a microchip (an array of immobilized mols., each including a DNA-protein fusion described here), identification of protein or compound-protein interaction, and protein display expts.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 8 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 2006-239063 [25] WPIDS
CROSS REFERENCE: 2004-045060 [05]
DOC. NO. CPI: C2006-078203
TITLE: Synthesizing copy of nucleic acid target, by annealing chimeric primer or chimeric nucleic acid construct that is complementary to target, with target, extending primer/nucleic acid construct using nucleic acid target as template.
DERWENT CLASS: B04 D16
INVENTOR(S): COLEMAN, J; DONEGAN, J J; RABBANI, E; STAVRIANOPOULOS, J G
PATENT ASSIGNEE(S): (COLE-I) COLEMAN J; (DONE-I) DONEGAN J J; (RABB-I) RABBANI E; (STAV-I) STAVRIANOPOULOS J G
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2006057583	A1	20060316	(200625)*		59

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2006057583	A1 CIP of	US 2001-896897	20010630
		US 2003-693481	20031024

PRIORITY APPLN. INFO: US 2003-693481 20031024; US 2001-896897 20010630

AN 2006-239063 [25] WPIDS
CR 2004-045060 [05]
AB US2006057583 A UPAB: 20060413

NOVELTY - Synthesizing (M1) copy of a nucleic acid target, by annealing chimeric primer or chimeric nucleic acid construct to nucleic acid target, where the primer or nucleic acid construct is complementary to nucleic acid target, and extending primer or nucleic acid construct by synthesizing reagents for the synthesis of a nucleic acid copy, using nucleic acid target as template to synthesize copy of nucleic acid target.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a composition (C1) of matter comprising set of nucleic acid constructs and permutational set of nucleic acid constructs;

(2) set of permutational primers (P1) or nucleic acid constructs;

(3) synthesizing (M2) one copy of **library** of nucleic acid targets;

(4) synthesizing (M3) one or more copies of a **library** of nucleic acid targets;

(5) synthesizing at least one nucleic acid target;

(6) synthesizing multiple copies of at least one nucleic acid target;

(7) synthesizing a double-stranded DNA copy from at least one RNA target;

(8) amplifying a **library** of nucleic acids; and

(9) adding nucleic acid sequences to a collection of target nucleic acids.

USE - (M1) is useful for synthesizing copy of nucleic acid target, preferably RNA and DNA target (claimed).

ADVANTAGE - (M1) is rapid and efficient. The copying or amplification of target nucleic acids can be carried out under conditions where synthesis (derived from target nucleic acid templates) is retained while potentially deleterious side reactions caused by nucleic acids acting inappropriately as either primers or as templates are avoided.

Dwg.0/13

L9 ANSWER 9 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 2005-214591 [22] WPIDS
DOC. NO. CPI: C2005-068657
TITLE: Determining the sequence of a target nucleic acid molecule, e.g. DNA molecule, comprises contacting the molecules with ligation cassettes comprising labeled oligonucleotide.
DERWENT CLASS: B04 D16
INVENTOR(S): BARNES, C
PATENT ASSIGNEE(S): (SOLE-N) SOLEXA LTD
COUNTRY COUNT: 108
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2005021786	A1	20050310	(200522)*	EN	33

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NA NL OA PL PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2005021786	A1	WO 2004-GB3666	20040827

PRIORITY APPLN. INFO: GB 2003-20059 20030827

AN 2005-214591 [22] WPIDS

AB WO2005021786 A UPAB: 20050406

NOVELTY - Determining the sequence of a target nucleic acid molecule comprises contacting the molecules with a **library** of ligation cassettes each comprising an oligonucleotide having one or more defined bases and having a characteristic label into it.

DETAILED DESCRIPTION - Determining the sequence of a target nucleic acid molecule comprises:

(a) immobilizing fragments of the target nucleic acid molecule onto the surface of a solid support to form an array of nucleic acid molecules which are capable of interrogation, each of the molecules being immobilized other than at that part of the molecule that can be

interrogated;

(b) contacting the molecules with a **library** of ligation cassettes each comprising an oligonucleotide having one or more defined bases and having a characteristic label into it, under conditions that permit ligation of one of the cassettes to a primer sequence hybridized or otherwise mainlined in a spatial relationship with the target nucleic acid molecules, each of the cassettes being blocked to permit only a single ligation event;

(c) identifying the characteristic label(s) attached to any ligated cassette and removing the blocking group associated into it and optionally removing the characteristic label; and

(d) repeating steps (a) to (c) for a number of times to generate a complementary oligonucleotide sequence to each of the target nucleic acid molecules, each of the complimentary oligonucleotide sequences having known nucleotides spaced intermittently along their length that can be placed in the context of a reference sequence and comparing the overlapping sequences of the oligonucleotide sequences in the context of the reference sequence Io determine the sequence of the target nucleic acid molecule.

USE - The method and cassettes are useful for determining the sequence of a target nucleic acid molecule, e.g. DNA molecule.

Dwg.0/6

L9 ANSWER 10 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 2005-163123 [17] WPIDS

DOC. NO. CPI: C2005-052787

TITLE: New oligomeric compound that can hybridize with or sterically interfere with nucleic acid molecules comprising or encoding small non-coding RNA targets, useful for treating e.g., cancer and diabetes.

DERWENT CLASS: B04 D16

INVENTOR(S): BAKER, B; BENNETT, C; BHAT, B; ESAU, C; FREIER, S; GRIFFEY, R; JAIN, R; KOLLER, E; LOLLO, B; MARCUSSON, E; PERALTA, E; SWAYZE, E; VICKERS, T; BAKER, B F; BENNETT, C F; FREIER, S M; GRIFFEY, R H; MARCUSSON, E G; SWAYZE, E E; VICKERS, T A

PATENT ASSIGNEE(S): (BAKE-I) BAKER B F; (BENN-I) BENNETT C F; (BHAT-I) BHAT B; (ESAU-I) ESAU C; (FREI-I) FREIER S M; (GRIF-I) GRIFFEY R H; (JAIN-I) JAIN R; (KOLL-I) KOLLER E; (LOLL-I) LOLLO B; (MARC-I) MARCUSSON E G; (PERA-I) PERALTA E; (SWAY-I) SWAYZE E E; (VICK-I) VICKERS T A; (ISIS-N) ISIS PHARM INC

COUNTRY COUNT: 109

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2005013901	A2	20050217	(200517)*	EN	854
RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NA NL OA PL PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW					
US 2005261218	A1	20051124	(200577)		
EP 1648914	A2	20060426	(200628)	EN	
R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IT LI LT LU LV MC MK NL PL PT RO SE SI SK TR					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE

WO 2005013901	A2		WO 2004-US25300	20040730
US 2005261218	A1	Provisional	US 2003-492056P	20030731
		Provisional	US 2003-516303P	20031031
		Provisional	US 2003-531596P	20031219
		Provisional	US 2004-562417P	20040414
			US 2004-909125	20040730
EP 1648914	A2		EP 2004-780181	20040730
			WO 2004-US25300	20040730

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1648914	A2 Based on	WO 2005013901

PRIORITY APPLN. INFO: US 2004-562417P 20040414; US 2003-492056P 20030731; US 2003-516303P 20031031; US 2003-531596P 20031219; US 2004-909125 20040730

AN 2005-163123 [17] WPIDS

AB WO2005013901 A UPAB: 20050311

NOVELTY - An oligomeric compound comprising a first region and a second region, where at least one region contains a modification, and a portion of the oligomeric compound is targeted to a small non-coding RNA target nucleic acid that is miRNA, or its precursor, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a composition comprising a first oligomeric compound and a second oligomeric compound, where at least one of the oligomeric compounds contains a modification, at least a portion of the first oligomeric compound is capable of hybridizing with at least a portion of the second oligomeric compound, and at least a portion of the first oligomeric compound is targeted to a small non-coding RNA target nucleic acid;

(2) a pharmaceutical composition comprising the composition cited above, and a carrier;

(3) a kit or assay device comprising the composition;

(4) modulating the expression of a small non-coding RNA target nucleic acid in a cell, tissue or animal;

(5) treating or preventing a disease or disorder associated with a small non-coding RNA target nucleic acid;

(6) treating a condition in an animal;

(7) treating or preventing a disease or disorder associated with CD36;

(8) methods of screening an oligomeric compound for an effect on miRNA signaling;

(9) methods of screening a miRNA precursor for an effect in miRNA signaling;

(10) methods of modulating translation, apoptosis, conversion of a precursor miRNA into miRNA, or cellular differentiation;

(11) identifying an RNA transcript bound to a small non-coding RNA;

(12) arresting or delaying entry of a cell at the G2/M phase;

(13) interfering with chromosome segregation;

(14) a method of triggering apoptosis;

(15) detecting a miRNA precursor;

(16) identifying a miRNA target;

(17) modulating cellular differentiation;

(18) treating a condition associated with adipocyte differentiation in an animal;

(19) treating or preventing a disease or disorder associated with aberrant regulation of the cell cycle by miRNAs;

(20) maintaining a pluripotent stem cell; and
(21) identifying a small non-coding RNA binding site.
ACTIVITY - Cytostatic; Antidiabetic; Anorectic; Antilipemic; Antiarteriosclerotic; Hypotensive; Neuroprotective; Nootropic; Antiangiogenic; Anabolic; Eating-Disorders-Gen.
Test details are described but no results are given.
MECHANISM OF ACTION - Gene therapy; RNA Interference.
USE - The compounds and compositions are useful for treating a disease or disorder resulting from chromosomal non-disjunction, altered methylation, acetylation, or pseudouridylation state of chromosomes, such as a hyperproliferative condition (e.g. cancer, neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity, hyperlipidemia, atherosclerosis, atherogenesis, hypertension, anorexia, Alzheimer's disease, a central nervous system injury or neurodegenerative disorder (all claimed).
Dwg.0/0

L9 ANSWER 11 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-699819 [68] WPIDS
CROSS REFERENCE: 2005-676854 [69]
DOC. NO. CPI: C2006-036495
TITLE: Synthesizing bifunctional complex useful for generating **library** of different bifunctional complexes having encoded molecules and identifier polynucleotides identifying chemical entities participated in synthesis of encoded molecule.
DERWENT CLASS: B04 D16
INVENTOR(S): FRANCH, T; GOULIAEV, A H; JACOBSEN, S N; NEVE, S; PEDERSEN, H; RASMUSSEN, T
PATENT ASSIGNEE(S): (NUEV-N) NUEVOLUTION AS
COUNTRY COUNT: 109
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004083427	A2	20040930	(200468)*	EN	127
RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PL PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW					
EP 1608748	A2	20051228	(200603)	EN	
R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HU IE IT LI LT LU LV MC MK NL PL PT RO SE SI SK TR					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004083427	A2	WO 2004-DK195	20040322
EP 1608748	A2	EP 2004-722237	20040322
		WO 2004-DK195	20040322

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1608748	A2 Based on	WO 2004083427

PRIORITY APPLN. INFO: US 2003-455858P 20030320; DK

AN 2004-699819 [68] WPIDS
CR 2005-676854 [69]
AB WO2004083427 A UPAB: 20060214

NOVELTY - Synthesizing (M1) bifunctional complex having encoded molecule and identifier polynucleotide capable of identifying chemical entities participated in synthesis of encoded molecule, where encoded molecule is generated by reacting at least two of several chemical entities associated with identifier polynucleotide, and the chemical entities are provided by separate building blocks.

DETAILED DESCRIPTION - Synthesizing (M1) comprises:

(a) a bifunctional complex comprising an encoded molecule and an identifier polynucleotide identifying the chemical entities having participated in the synthesis of the encoded molecule, involves:

(i) providing at least one template comprising one or more codons capable of hybridizing to an anticodon, where the template is optionally associated with one or more chemical entities, and several building blocks each comprising an anticodon associated with one or more chemical entities;

(ii) hybridizing the anticodon of one or more of the provided building blocks to the template;

(iii) covalently linking the anticodons and/or linking the at least one template with the anticodon of at least one building block, thus generating an identifier polynucleotide capable of identifying chemical entities having participated in the synthesis of the encoded molecule;

(iv) separating the template from one or more of the anticodons hybridized to it, thus generating an at least partly single stranded identifier polynucleotide associated with several chemical entities; and

(v) generating a bifunctional complex comprising an encoded molecule and an identifier polynucleotide identifying the chemical entities having participated in the synthesis of the encoded molecule, where the encoded molecule is generated by reacting at least two of the several chemical entities associated with the identifier polynucleotide, where the at least two chemical entities are provided by separate building blocks;

(b) one or more bifunctional complexes each comprising a molecule resulting from the reaction of several of chemical entities and an identifier polynucleotide identifying one or more of the chemical entities having participated in the synthesis of the molecule, involves:

(i) providing several of building blocks each comprising an oligonucleotide associated with one or more chemical entities;

(ii) providing at least one connector oligonucleotide capable of hybridizing with one or more building block oligonucleotides;

(iii) immobilizing at least one building block to a solid support;

(iv) hybridizing the immobilized building block oligonucleotide to a first connector oligonucleotide;

(v) hybridizing at least one additional building block oligonucleotide to the first connector oligonucleotide;

(vi) ligating building block oligonucleotides hybridized to the connector oligonucleotide;

(vii) separating the connector polynucleotide from the ligated building block oligonucleotides; and

(viii) reacting one or more chemical entities associated with different building block oligonucleotides, thus obtaining a first bifunctional complex comprising a first molecule or first molecule precursor linked to a first identifier oligonucleotide identifying the chemical entities having participated in the synthesis of the molecule or molecule precursor, where the first bifunctional complex is immobilized to a solid support;

(c) a bifunctional complex comprising a molecule resulting from the reaction of several of chemical entities, where the molecule is linked to an identifier polynucleotide identifying one or more of the chemical entities having participated in the synthesis of the molecule; or

(d) a bifunctional complex comprising an encoded molecule and a template coding for one or more chemical entities which have participated in the synthesis of the encoded molecule.

An INDEPENDENT CLAIM is also included for a **library** (I) of different complexes, each complex comprising an encoded molecule and a template, which has encoded the chemical entities, which has participated in its synthesis, and the **library** being obtainable by processing several different templates and several building blocks by (M1).

USE - (M1a) is useful for generating a **library** of different bifunctional complexes, which involves repeating the steps of (M1a) using a different combination of building blocks and templates for each repetition. The method further involves converting the identifier polynucleotides into duplex molecules each comprising complementary identifier oligonucleotides identifying the chemical entities having participated in the synthesis of the encoded molecule of a bifunctional complex. The template part of the identifier oligonucleotide is separated from the encoded molecule prior to amplification. The method further involves displacing complementary identifier oligonucleotides, thus generating a population of heterogeneous identifier oligonucleotides, and re-annealing the displaced identifier oligonucleotides under conditions where homo-duplexes and hetero-duplexes are formed, where homo-duplexes comprises identifier oligonucleotides originating from identical bifunctional complexes, and where hetero-duplexes comprises identifier oligonucleotides originating from different bifunctional complexes, such as bifunctional complexes comprising different encoded molecules. The homo-duplexes and hetero-duplexes are separated by a chemical or enzymatic separation methods, or by physical separation methods. The homo-duplexes are isolated by removal of hetero-duplexes. The hetero-duplexes are removed by enzymatic degradation. The enzyme comprises a nuclease activity. The enzyme is chosen from T4 endonuclease VII, T4 endonuclease I, nuclease S1, CEL I or their variants. The enzyme is thermostable. The **library** comprises 1,000 or more different members, such as 105 or 1012 different members. The molecular target is immobilized on a solid support. The target immobilized on the support forms a stable or quasi-stable dispersion. The molecular target comprises an antibody, a nucleic acid such as DNA aptamer or RNA aptamer, or a polypeptide such as kinases, proteases or phosphatases. The target polypeptide is attached to a nucleic acid having templated the synthesis of the polypeptide. Any remaining homo-duplexes are amplified prior to decoding the identity of the encoded molecule of a bifunctional complex. The steps of identifier oligonucleotide displacement and re-annealing are repeated at least once. The identifier oligonucleotides comprising codons and/or anticodons are recovered from the selection procedure and reused for a second or further round synthesis of encoded molecules (all claimed).

DESCRIPTION OF DRAWING(S) - The figure is a schematic representation of a general method for producing an encoded molecule using stepwise ligation and stepwise reaction of chemical entities.

Dwg.1/12

L9 ANSWER 12 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-635552 [61] WPIDS
CROSS REFERENCE: 2004-652966 [63]; 2005-233512 [24]
DOC. NO. CPI: C2004-228439
TITLE: Producing a second-generation **library** of molecules with improved desired property using an initial **library** with a plurality of encoded molecules associated with an identifier nucleic acid sequence.
DERWENT CLASS: B04 D16
INVENTOR(S): FRESKGARD, P; GOULIAEV, A H; OLSEN, E K; THISTED, T
PATENT ASSIGNEE(S): (NUEV-N) NUEVOLUTION AS
COUNTRY COUNT: 109
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004074429	A2	20040902	(200461)*	EN	118

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

EP 1597395	A2	20051123	(200577)	EN	

R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HU IE IT LI LT LU LV MC MK NL PT RO SE SI SK TR

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004074429	A2	WO 2004-DK117	20040223
EP 1597395	A2	EP 2004-713517	20040223
		WO 2004-DK117	20040223

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1597395	A2 Based on	WO 2004074429

PRIORITY APPLN. INFO: US 2003-504748P 20030922; DK
2003-268 20030221; DK
2003-269 20030221; US
2003-448460P 20030221; US
2003-448480P 20030221; DK
2003-1356 20030918

AN 2004-635552 [61] WPIDS

CR 2004-652966 [63]; 2005-233512 [24]

AB WO2004074429 A UPAB: 20051130

NOVELTY - Producing composition of molecules with improved desired property comprises providing an initial **library** comprising many different encoded molecules associated with a corresponding identifier nucleic acid sequence, subjecting the **library** to condition partitioning members, identifying codons of the identifier nucleic acids of the partitioned members of the initial **library**, and preparing a second-generation **library** of encoded molecules.

DETAILED DESCRIPTION - Producing a composition of molecules with an improved desired property comprises providing an initial **library** comprising a plurality of different encoded molecules associated with a corresponding identifier nucleic acid sequence, where each encoded molecule comprises a reaction product of multiple chemical entities and the identifier nucleic acid sequence comprises codons identifying the chemical entities, subjecting the initial **library** to a condition partitioning members having encoded molecules displaying a predetermined property from the remainder of the initial **library**, identifying codons of the identifier nucleic acid sequences of the partitioned members of the initial **library**, and preparing a second-generation **library** of encoded molecules using the chemical entities coded for by the codons of the partitioned members of the initial **library** or its part.

INDEPENDENT CLAIMS are also included for the following:

(1) a composition of molecules with an improved desired property, obtainable by the method cited above; and

(2) a molecule identifiable by subjecting a composition of molecules obtainable by the method cited above to a condition partitioning members having encoded molecules displaying a predetermined property from the remainder of the composition, and identifying the partitioned encoded molecule(s).

USE - The methods and compositions of the present invention are useful for producing a second-generation compound **library** with an improved desired property profile and lower diversity.

Dwg.0/17

L9 ANSWER 13 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-757005 [71] WPIDS
DOC. NO. CPI: C2003-207843
TITLE: New naked nucleic acid-virion protein display complex useful in functional genomics, proteomics and in protein identification for the exploration of therapeutic drugs and new diagnostic procedures.
DERWENT CLASS: B04 D16
INVENTOR(S): LINDQVIST, B H
PATENT ASSIGNEE(S): (LIND-I) LINDQVIST B H
COUNTRY COUNT: 103
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2003078628	A1	20030925	(200371)*	EN	31
RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO NZ OM PH PL PT RO RU SC SD SE SG SK SL TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW					
NO 2002001298	A	20030916	(200371)		
AU 2003212720	A1	20030929	(200432)		
US 2006003314	A1	20060105	(200603)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003078628	A1	WO 2003-NO88	20030313
NO 2002001298	A	NO 2002-1298	20020315
AU 2003212720	A1	AU 2003-212720	20030313
US 2006003314	A1	WO 2003-NO88	20030313
		US 2005-507434	20050824

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2003212720	A1 Based on	WO 2003078628

PRIORITY APPLN. INFO: NO 2002-1298 20020315
AN 2003-757005 [71] WPIDS
AB WO2003078628 A UPAB: 20031105

NOVELTY - A display virus complex exposing a naked nucleic acid comprising an exogenous nucleic acid and its encoded peptide or polypeptide, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) preparing covalently linked naked nucleic acid-protein display complexes from virus particles cited above, comprising:

(a) treating a freshly prepared virus preparation with cross-linking chemical agents producing covalently linked naked nucleic acid-virus protein display complexes; and

(b) coupling of the naked nucleic acid-virus protein display complexes to a solid support by hybridizing the naked nucleic acid-virus protein display complexes against a complementary nucleic acid sequence in an array format, where the hybridization leads to positioning the displayed protein/peptide to its own gene or related gene(s); and

(2) a kit comprising the virus display complex cited above.

USE - The display virus complex and method are useful in functional genomics, proteomics and in protein or peptide identification for the exploration of therapeutic drugs as well as in search for new diagnostic procedures (claimed).

The naked nucleic acid-virion protein display complex may also be used as a scaffold for bi-functional display after nucleic acid hybridization of 2 different display complexes.

Dwg.0/8

L9 ANSWER 14 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 2002-055473 [07] WPIDS

DOC. NO. CPI: C2002-015889

TITLE: Selecting adenylate uridylate-rich element (ARE) coding sequences from databases, comprises extracting nucleic acids with protein coding sequences upstream, contiguous with a 3' untranslated region having a specific ARE sequence.

DERWENT CLASS: B04 D16

INVENTOR(S): ABU-KHABAR, K S; FREVEL, M; SILVERMAN, R H; WILLIAMS, B R G

PATENT ASSIGNEE(S): (CLEV-N) CLEVELAND CLINIC FOUND; (KING-N) KING FAISAL SPECIALIST HOSPITAL & RES CE; (ABUK-I) ABU-KHABAR K S; (FREV-I) FREVEL M; (SILV-I) SILVERMAN R H; (WILL-I) WILLIAMS B R G

COUNTRY COUNT: 95

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001083691	A2	20011108	(200207)*	EN	106
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2001055344	A	20011112	(200222)		
US 2004023231	A1	20040205	(200411)		
EP 1410301	A2	20040421	(200427)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE TR					
JP 2004524801	W	20040819	(200455)		194

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001083691	A2	WO 2001-US11993	20010412
AU 2001055344	A	AU 2001-55344	20010412
US 2004023231	A1	WO 2001-US11993	20010412
		US 2003-257294	20030714
EP 1410301	A2	EP 2001-928494	20010412
		WO 2001-US11993	20010412
JP 2004524801	W	JP 2001-580301	20010412

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2001055344	A Based on	WO 2001083691
EP 1410301	A2 Based on	WO 2001083691
JP 2004524801	W Based on	WO 2001083691

PRIORITY APPLN. INFO: US 2000-196870P 20000412; US 2003-257294 20030714

AN 2002-055473 [07] WPIDS

AB WO 200183691 A UPAB: 20020130

NOVELTY - Selecting nucleic acids (NA) involves extracting protein coding sequences (PCS) from a database which contains several NA, each of which comprises full-length or partial PCS and a 3' untranslated region (UTR) sequence downstream and contiguous with PCS, by identifying PCS located upstream and contiguous with a 3' UTR which has an adenylate uridylate-rich element (ARE) search sequence.

DETAILED DESCRIPTION - Selecting (M1) a set of nucleic acids for analyzing expression in a cell, by:

(a) providing a database containing several NA, each comprising a full-length or partial PCS and a 3' UTR sequence downstream and contiguous with the PCS;

(b) extracting a set of the PCS from the database by identifying PCS located upstream and contiguous with a 3' UTR which comprises 1 of the following target sequences (ARE search sequences) (TS):

(i) a target sequence, WU/T(AU/TU/TU/TA)U/TWWW, where 0 or 1 of the nucleotides outside of the parenthesis is replaced by a different nucleotide, and where W represents A, U or T; or

(ii) a second target sequence, U/T(AU/TU/TU/T)n, where n indicates that the second target sequence comprises from 3 to 12 of the tetrameric sequences within the parenthesis.

INDEPENDENT CLAIMS are also included for the following:

(1) preparing (M2) a **library** (I) of NA for analyzing gene expression in a cell;

(2) a NA **library** (I);

(3) preparing (M3) a customized array (II) for analyzing expression of ARE genes in a cell by:

(i) determining the PCS of the NA selected by (M1); and

(ii) attaching a gene probe for each of the NA to a solid support to provide the array;

(4) a customized array (II);

(5) extracting (M4) ARE genes from a genomic database by:

(i) identifying genomic regions comprising an ARE motif;

(ii) locating the protein coding regions upstream of the genomic region; and

(iii) subjecting the genomic region to the computer gene prediction program;

(6) identifying (M5) primers sets targeted to the initiation region of genes whose 3'UTR comprise ARE sequences by:

(a) locating the start codon of PCS of genes whose 3' UTR comprise TS;

(b) grouping the genes into 4 classes, given in the specification; and

(c) constructing a consensus sequence for each of the classes; or

(d) grouping (M6) the genes into 1 of 16 classes, given in the specification;

(7) selectively amplifying (M7) ARE-gene transcripts, by:

(a) reverse transcribing RNA molecules obtained from a cell which is expressing ARE-genes to provide a pool of single-stranded DNA molecules;

(b) amplifying a portion of the ARE-containing DNA molecules within the pool by a polymerase chain reaction (PCR) which employs:

(i) a 3' primer, 13 to 50 nucleotides in length and comprising 2 to 10 pentamers of TAAAT, where the pentameric sequences are overlapping or non-overlapping; and

(ii) primers encompassed by 1 of the 5' primer sets obtained according to (M5) or (M6); or

(c) reverse transcribing (M8) the RNA obtained from a cell to provide a pool of single-stranded DNA molecules using a reverse transcriptase and a 3' primer,13 to 50 nucleotides in length and comprising 2 to 10 (overlapping or non-overlapping) pentamers with the sequence TAAAT;

(d) amplifying the ARE-containing DNA molecules within the pool by a PCR;

(8) selectively (M9) amplifying ARE-gene transcripts by:

(a) reverse transcribing RNA molecules obtained from a cell expressing ARE-genes to provide a pool of single-stranded cDNA molecules;

(b) ligating an oligomer to the cDNA molecules, where the oligomer is 50-70 nucleotides in length, is phosphorylated at its 3' end and protected at its 5' end with an NH2, and has a sequence which does not hybridize under stringent conditions to human mRNA molecules;

(c) PCR amplifying the ARE-containing DNA molecules within the cDNA molecules using:

(i) a 3' primer, 3 to 50 nucleotides in length and comprising 2 to 10 pentamers of TAAAT, where the pentameric sequences are overlapping or non-overlapping, and

(ii) a 5' primer identical to a sequence contained within a oligomer;

(9) preparing (M10) a library (IV) of NA for analyzing gene expression in a cell by:

(i) obtaining NA whose PCS have been identified according to (M7)-(M9) where the PCS of each of the NA is different; and

(ii) incorporating each of the NA into a separate NA vector to provide the library;

(10) a NA library (IV);

(11) preparing (M11) a customized array (V) for analyzing expression of ARE genes in a cell by:

(i) determining PCS of ARE NAs amplified according to (M7), (M8), (M9);

(ii) attaching a gene probe for each of the NA to a solid support to provide the array, where each probe (an oligonucleotide, a cDNA molecule or a synthetic gene probe) hybridizes under stringent conditions to a target region within the PCS or its complement; and

(12) a customized array (V).

USE - The method is used for selecting a set of NAs for analyzing gene expression in a cell. Nucleic acids selected by (M1) are useful for preparing a customized array of ARE genes which involves:

(a) identifying a group of unique sequence with a PCS of ARE genes selected according to (M1);

(b) preparing a set of oligonucleotides or polynucleotides, where each polynucleotide or oligonucleotide in the set comprises one of the unique sequences in the group; and

(c) attaching the oligonucleotides or polynucleotides to a solid support.

The microarrays produced are useful for obtaining an ARE expression profile in a subject which involves extracting RNA from a tissue sample obtained from the subject, labeling the RNA with a detectable tag, contacting the labeled RNA with a microarray, and determining the sequence or pattern of the labeled RNA molecules which hybridize under stringent conditions with the probes present on the microarray (claimed). The microarrays are useful for obtaining an ARE expression profile, particularly a subject with a disease such as cancer. The ARE genes identified by the above mentioned method are useful for generation of polymerase chain reaction (PCR) products or oligonucleotides for use as

immobilized probes in cDNA or oligonucleotide microarrays, respectively. Dwg.0/7

L9 ANSWER 15 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2001-657558 [76] WPIDS
CROSS REFERENCE: 2001-425661 [45]; 2002-010801 [01]
DOC. NO. CPI: C2001-193639
TITLE: Parallel sequencing of several nucleic acids, useful e.g. in gene expression analysis, using irreversibly immobilized amplification primers.
DERWENT CLASS: B04 D16
INVENTOR(S): FISCHER, A
PATENT ASSIGNEE(S): (AXAR-N) AXARON BIOSCIENCE AG; (BADI) BASF-LYNX BIOSCIENCE AG
COUNTRY COUNT: 2
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
DE 10016348	A1	20011004	(200176)*		30
AU 2001254771	A8	20051006	(200612)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
DE 10016348	A1	DE 2000-10016348	20000403
AU 2001254771	A8	AU 2001-254771	20010403

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2001254771	A8 Based on	WO 2001075154

PRIORITY APPLN. INFO: DE 2000-10016348 20000403; DE 2000-10051564 20001018
AN 2001-657558 [76] WPIDS
CR 2001-425661 [45]; 2002-010801 [01]
AB DE 10016348 A UPAB: 20060217
NOVELTY - Parallel sequencing of at least two different nucleic acids (NA), present in a mixture, is new.

DETAILED DESCRIPTION - Parallel sequencing of at least two different nucleic acids (NA), present in a mixture. At least one pair of primers is immobilized irreversibly on a surface and treated with an NA mixture containing molecules that can hybridize to both primers. The immobilized primers are extended, in complementary fashion, to form a counter strand, resulting in formation of secondary NA (sNA). The surface is freed of NA that is not irreversibly bound and the sNA amplified to form tertiary nucleic acid (tNA). Counter-strands (gtNA) of tNA are prepared and extended by a single nucleotide (nt) in which the 2'- or 3'-hydroxy is protected, and which is detectably labeled. The incorporated nt is identified, the protecting group removed and the label either removed or altered. The single-nt extension procedure is repeated until the required sequence information has been obtained.

INDEPENDENT CLAIMS are also included for the following:

(1) similar method in which tNA is treated so that it is bound to the surface only through the 5'-end of one strand, then cut with a type IIS restriction enzyme (RE) to generate 3' or 5' overhangs, determining one or more bases in these overhangs, ligating linkers to the free ends (these linkers include a recognition site for type IIS RE), treating again with RE that recognizes the site introduced in the linker and repeating the

process as required;

(2) apparatus for performing the new process;

(3) method for localized amplification of NA, comprising the new process as far as amplification to produce tNA; and

(4) surface-bound **library** of NA produced by the method for localized amplification of NA.

USE - The method is useful for detecting genes and transcripts (e.g. for expression analysis), identifying mutations and polymorphisms, and detecting organisms and viruses.

ADVANTAGE - The method provides highly parallel sequencing, requires relatively small amounts of DNA, can sequence long segments and does not require complex apparatus.

Dwg.0/13

L9 ANSWER 16 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 1999-539985 [45] WPIDS

DOC. NO. CPI: C1999-157718

TITLE: 5' nuclease amplification assay using fluorescence-quencher probes for determination of a genotype at multiple allelic sites.

DERWENT CLASS: A11 A28 A96 A97 B04 D16

INVENTOR(S): GOODSAID, F; LIVAK, K J

PATENT ASSIGNEE(S): (APPL-N) APPLERA CORP; (PEKE) PERKIN-ELMER CORP; (GOOD-I) GOODSAID F; (LIVA-I) LIVAK K J; (PEKE) PE APPLIED BIOSYSTEMS INC

COUNTRY COUNT: 23

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9940226	A2	19990812	(199945)*	EN	95
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: AU CA JP					
US 5962233	A	19991005	(199948)		
AU 9923144	A	19990823	(200005)		
EP 1053348	A2	20001122	(200061)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
US 6154707	A	20001128	(200063)		
JP 2002502615	W	20020129	(200211)		92
US 2002164630	A1	20021107	(200275)		
AU 758463	B	20030320	(200329)		
US 2004053302	A1	20040318	(200421)		
AU 2003204856	A1	20030724	(200464)#		
US 6884583	B2	20050426	(200528)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9940226	A2		WO 1999-US499	19990108
US 5962233	A		US 1998-18595	19980204
AU 9923144	A		AU 1999-23144	19990108
EP 1053348	A2		EP 1999-903026	19990108
			WO 1999-US499	19990108
US 6154707	A	Div ex	US 1998-18595	19980204
			US 1999-324709	19990603
JP 2002502615	W		WO 1999-US499	19990108
			JP 2000-530635	19990108
US 2002164630	A1	Cont of	US 1998-18595	19980204
			US 2002-104774	20020321
AU 758463	B		AU 1999-23144	19990108
US 2004053302	A1	Div ex	US 1998-18595	19980204

		Cont of	US 1999-326828	19990603
			US 2003-455150	20030604
AU 2003204856	A1	Div ex	AU 1999-23144	19990108
			AU 2003-204856	20030620
US 6884583	B2	Cont of	US 1998-18595	19980204
			US 2002-104774	20020321

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9923144	A	Based on	WO 9940226
EP 1053348	A2	Based on	WO 9940226
JP 2002502615	W	Based on	WO 9940226
AU 758463	B	Previous Publ.	AU 9923144
		Based on	WO 9940226

PRIORITY APPLN. INFO: US 1998-18595 19980204; US 1999-324709 19990603; US 2002-104774 20020321; US 1999-326828 19990603; US 2003-455150 20030604; AU 2003-204856 20030620

AN 1999-539985 [45] WPIDS

AB WO 9940226 A UPAB: 20011203

NOVELTY - First and second sets of fluorescer-quencher probes are used simultaneously in a 5' nuclease assay to identify which members of a first or second set of substantially homologous sequences are present in a DNA sample.

DETAILED DESCRIPTION - Identifying which members of two or more sets of substantially homologous sequences are present in a sample of DNA, comprises:

(a) performing nucleic acid amplification on a DNA sample, which includes a first set of substantially homologous sequences and a second, different set of substantially homologous sequences using:

(i) a nucleic acid polymerase having 5' to 3' nuclease activity; and

(ii) one or more sets of forward and reveres primers capable of hybridizing to the sample DNA, in the presence of two or more sets of oligonucleotide probes;

(b) amplifying the sets of substantially homologous sequences, where:

(i) each set of substantially homologous sequences includes two or more members which each differ from each other at, at least, one base position;

(ii) each set of oligonucleotide probes is for detecting the members of one of the sets of substantially homologous sequences;

(iii) each set of oligonucleotide probes includes two or more probes which are complementary to different members of a set of substantially homologous sequences, the member being 5' relative to a sequence of the sample DNA to which the primer hybridizes; and

(iv) at least all but one of the oligonucleotide probes include a different fluorescer than the other probes and a quencher positioned on the probe to quench the fluorescence of the fluorescer;

(c) digesting those oligonucleotide probes which hybridize to the target sequence during the amplification by the nuclease activity of the polymerase;

(d) detecting a fluorescence spectrum of the amplification;

(e) calculating a fluorescence contribution of each fluorescer to the fluorescence spectrum; and

(f) determining a presence or absence of the different members of substantially homologous sequences based on the fluorescence contribution of each fluorescer to the fluorescence spectrum.

INDEPENDENT CLAIMS are also included for the following:

(1) genotyping a sample of DNA at, at least, two allelic sites by a 5' nuclease amplification reaction;

(2) a fluorescence spectrum or signature (or **library** of fluorescence signatures) for genotyping a sample of DNA at, at least, two allelic sites;

(3) determining a fluorescence signature of a samples of DNA;

(4) genotyping a sample of DNA at two or more different allelic sites;

(5) a processor for genotyping a sample of DNA at, at least, two allelic sites by a 5' nuclease assay; and

(6) kits for the above methods.

USE - The methods can be used to genotype a sample of genomic DNA at two or more different allelic sites. Generating a fluorescence spectrum and signature for each genotype, which uniquely reflects the assay's inherent inefficiency for that genotype given the particular conditions, probes and primers used, the genotype of unknown sequences can be determined. The assay was shown to be useful for determining apoE genotypes. The assay can be used as a diagnostic tool for assessing the risk for coronary artery disease and/or late-onset Alzheimer's disease.

ADVANTAGE - Using the 5' nuclease assay of the invention it is possible to determine a genotype at two or more allelic sites in a single reaction. This approach is much faster than previous approaches to genotyping genes having two or more allelic sites, such as the apolipoprotein E gene. A key advantage of the method for determining the genotype of a sample of DNA at multiple allelic sites is that it does not rely on 5' nuclease assay working with 100% efficiency to distinguish between substantially homologous sequences such as alleles.

Dwg.0/15

L9 ANSWER 17 OF 17 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 1996-383661 [38] WPIDS

CROSS REFERENCE: 1998-158364 [14]; 1999-253851 [21]; 2001-637949 [62]

DOC. NO. CPI: C1996-120737

TITLE: Nucleic acid amplification, detection and synthesis methods - using primer-promoter complex, where primer is responsible for synthesis of 1st and 2nd strands, the transcription of which is initiated by promoter.

DERWENT CLASS: B04 D16

INVENTOR(S): BARCHAS, J D; EBERWINE, J H; VAN GELDER, R N; VON ZASTROW, M E

PATENT ASSIGNEE(S): (BARC-I) BARCHAS J D; (EBER-I) EBERWINE J H; (VGEL-I) VAN GELDER R N; (VZAS-I) VON ZASTROW M E

COUNTRY COUNT: 1

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 5545522	A	19960813	(199638)*		12

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
US 5545522	A	Cont of	US 1989-411370	19890922
			US 1992-957647	19921005

PRIORITY APPLN. INFO: US 1989-411370 19890922; US 1992-957647 19921005

AN 1996-383661 [38] WPIDS

CR 1998-158364 [14]; 1999-253851 [21]; 2001-637949 [62]

AB US 5545522 A UPAB: 20011217

Amplifying at least 1 target nucleic acid sequence using a single species of **primer** complex, comprises: (a) synthesising a nucleic acid by hybridising the **primer** complex to the target sequence and extending the **primer** complex to form a 1st strand complementary to the target sequence, and synthesising a 2nd strand complementary to the 1st strand, where synthesis of the 2nd strand is primed by a **hairpin** loop formed spontaneously at the 3' end of the 1st strand; and (b) transcribing copies of RNA complementary to the 2nd strand initiated from the promoter region of the **primer** complex.

USE - The methods can be used for the amplification of a target nucleic acid, detecting the expression of a gene in a cell population, producing a subtractive hybridisation probe, making a cDNA **library** from a collection of mRNA mols., utilising a single primer complex for amplifying a nucleic acid sequence and amplifying mRNA in single brain cells, respectively.

Dwg.0/1

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=> d his

     (FILE 'HOME' ENTERED AT 19:01:58 ON 06 JUN 2006)

     FILE 'MEDLINE, BIOSIS, CAPLUS, SCISEARCH, EMBASE, WPIDS' ENTERED AT
     19:02:22 ON 06 JUN 2006
L1             5 SIRNA AND LIBRAR? AND RANDOM? AND (HAIRPIN (S) PRIMER)
L2             4 DUP REM L1 (1 DUPLICATE REMOVED)
L3            13 LIBRAR? AND RANDOM? AND (HAIRPIN (S) PRIMER)
L4            11 DUP REM L3 (2 DUPLICATES REMOVED)
L5             9 L3 NOT L2
L6            43 LIBRAR? AND (HAIRPIN (S) PRIMER)
L7            28 DUP REM L6 (15 DUPLICATES REMOVED)
L8            17 L7 NOT L3
L9            17 L8 NOT L2

=> FIL STNGUIDE
COST IN U.S. DOLLARS                            SINCE FILE      TOTAL
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FULL ESTIMATED COST                                188.67     188.88

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)      SINCE FILE      TOTAL
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CA SUBSCRIBER PRICE                                -3.75      -3.75

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FULL ESTIMATED COST                                  0.18     189.06

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)      SINCE FILE      TOTAL
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